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RESULT 12

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DEFINITION Sequence 1 from patent US 6149903.
ACCESSION ARL18507
VERSION ARL18507.1 GI:14100417
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,
Jettont,T.L., Robinson-Benion,C.L. and Thompson,M.E.
TITLE Characterized BRCA1 and BRCA2 proteins and screening and
therapeutic methods based on characterized BRCA1 and BRCA2 proteins
JOURNAL Patent: US 6149903-A 1 21-NOV-2000;
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source Location/Qualifiers
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ORIGIN

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Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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JOURNAL	Patent: US 6177410-A 1 23-JAN-2001;		
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ACCESSION AR184044
VERSION AR184044.1 GI:2028013
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SOURCE Unknown.
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REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S.,
Robinson-Benion,C.L. and Thompson,M.E.
TITLE Method for detection and treatment of breast cancer
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LOCUS      AR004673
DEFINITION Sequence 1 from patent US 5747282.
ACCESSION AR004673
VERSION    AR004673.1 GI:3965552
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
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AUTHORS   Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
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           and Futreal,P.Andrew.
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Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*1: geneseqn1980s:.*
2: geneseqn1980s:.*
3: geneseqn2000s:.*
4: geneseqn2000s:.*
5: geneseqn2000s:.*
6: geneseqn2000s:.*
7: geneseqn2000s:.*
8: geneseqn2000s:.*
9: geneseqn2000s:.*
10: geneseqn2000s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5589	100.0	5711	2	AAV46450 Human BRC
2	5589	100.0	5711	2	AAV46450 Human BRC
3	5589	100.0	5711	8	AAV46450 Human BRC
4	5589	100.0	5711	9	AAV46450 Human BRC
5	5588.6	100.0	5711	2	AAV46450 Human BRC
6	5588.6	100.0	5711	2	AAV46450 Human BRC
7	5588.6	100.0	5711	2	AAV46450 Human BRC
8	5588.6	100.0	5711	2	AAV46450 Human BRC
9	5588.6	100.0	5711	2	AAV46450 Human BRC
10	5588.6	100.0	5711	2	AAV46450 Human BRC
11	5588.6	100.0	5711	2	AAV46450 Human BRC
12	5588.6	100.0	5711	2	AAV46450 Human BRC
13	5587.4	100.0	5711	2	AAV46450 Human BRC
14	5587.4	100.0	5711	2	AAV46450 Human BRC
15	5587.4	100.0	5711	2	AAV46450 Human BRC
16	5587.4	100.0	5711	3	AAV46450 Human BRC
17	5587.4	100.0	5711	8	AAV46450 Human BRC
18	5587.4	100.0	5711	9	AAV46450 Human BRC
19	5587.4	100.0	5711	2	AAV46450 Human BRC
20	5587.4	100.0	5711	2	AAV46450 Human BRC
21	5587.4	100.0	5711	2	AAV46450 Human BRC
22	5587.4	100.0	5711	2	AAV46450 Human BRC
23	5587.4	100.0	5711	2	AAV46450 Human BRC

24	5587	100.0	5711	2	AAV46450
25	5585.8	99.9	5711	7	ACD25993
26	5582.2	99.9	5711	2	AAV46459
27	5582.2	99.9	5711	2	AAV46464
28	5582.2	99.9	5711	2	AAV46462
29	5582.2	99.9	5711	2	AAV46461
30	5581	99.9	5711	2	AAV46449
31	5581	99.9	5711	3	AAV46495
32	5581	99.9	5711	8	AAV46434
33	5581	99.9	5711	2	AAV46434
34	5581	99.9	5711	2	AAV46434
35	5581	99.9	5711	2	AAV46434
36	5581	99.9	5711	2	AAV46434
37	5581	99.9	5711	2	AAV46434
38	5580.6	99.8	5711	2	AAV46458
39	5580.6	99.8	5711	2	AAV46458
40	5580.6	99.8	5711	2	AAV46458
41	5579.4	99.8	5711	7	AB223502
42	5579.4	99.8	5712	2	AAV46480
43	5579.4	99.8	5712	3	AAV46480
44	5579.4	99.8	5714	2	AAV46480
45	5579.4	99.8	5714	2	AAV46480

ALIGNMENTS

RESULT 1
AAV46450
ID AAV46450 standard; cDNA; 5711 BP.
XX
AC AAV46450:
DT 18-NOV-1998 (first entry)
XX Human BRCA1 omi3 cDNA.
XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 120..5711
XX /*tag= a
XX /*product= "BRCA1 omi3 protein"
XX US5750400-A.
XX 12-MAY-1998.
XX 12-FEB-1997; 97US-00798691.
XX 12-FEB-1996; 96US-00598591.
XX (ONCO-) ONCORMED INC.
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Scheiter DB, Allen AC;
XX Critz BS;
XX WPI: 1998-296774/26.
XX P-PSDB; AAV76100.
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.
XX Claim 2e; Col 55-62; 54pp; English.
XX This sequence encodes the human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi3 gene. This sequence and polymorphic variations of
XX this sequence are useful for the identification of an individual who may

1981 AGGCCAGCAGCAAACTCACAACCTATGGAAGGTAAAGAACCTGCACCTGAGCCCAAGAG 2040
DB AGGCCAGCAGCAAACTCACAACCTATGGAAGGTAAAGAACCTGCACCTGAGCCCAAGAG 2159
2041 AGTACACGCCCAATCAACAGCAAGCTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2100
DB AGTACACGCCCAATCAACAGCAAGCTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2219
2160 AGTAAACCAAGCCAAATGAACAGCAAGCTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2160
DB AGTAAACCAAGCCAAATGAACAGCAAGCTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2279
2101 AAGTTAAACAAATGCACCTGCTTTCTTTACTAAGTGTTCAAATAACAGTGAACCTTAAAGAA 2160
DB AAGTTAAACAAATGCACCTGCTTTCTTTACTAAGTGTTCAAATAACAGTGAACCTTAAAGAA 2279
2161 TTGTGCAATCTAGCCTTCCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2220
DB TTGTGCAATCTAGCCTTCCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2339
2280 TTGTGCAATCTAGCCTTCCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2280
DB TTGTGCAATCTAGCCTTCCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2399
2221 TCTAATAATGCTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2340
DB TCTAATAATGCTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2459
2281 GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATGACACTCAG 2400
DB GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATGACACTCAG 2519
2341 GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATGACACTCAG 2460
DB GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATGACACTCAG 2579
2401 TGTGTGAGTCAAGTGTGCAAGTGTGAAACCCCAAGGGCTAATTTCACTGGTGTTCGAA 2520
DB TGTGTGAGTCAAGTGTGCAAGTGTGAAACCCCAAGGGCTAATTTCACTGGTGTTCGAA 2639
2461 GATAATAGAAATGACACAGAGCTTTAAGTATCTCAATGGGACATCAAGTTAAGCACTG 2580
DB GATAATAGAAATGACACAGAGCTTTAAGTATCTCAATGGGACATCAAGTTAAGCACTG 2699
2521 CGGGAACCAAGCAATGAAATGGAAGAAAGTGAACCTTGATCTCAGTATTTGCAAGATACA 2640
DB CGGGAACCAAGCAATGAAATGGAAGAAAGTGAACCTTGATCTCAGTATTTGCAAGATACA 2759
2581 TTCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGGAAATGCAAGAGAG 2700
DB TTCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGGAAATGCAAGAGAG 2819
2641 GAATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACT 2760
DB GAATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACT 2879
2701 TTGAAATGTGAACAAAGGAAGAAATCAAGGAAGAAATCAAGGAAGAAATCAAGGAAGAAAT 2820
DB TTGAAATGTGAACAAAGGAAGAAATCAAGGAAGAAATCAAGGAAGAAATCAAGGAAGAAAT 2939
2761 CAGACAGTTAAATCACTCAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2880
DB CAGACAGTTAAATCACTCAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2999
2880 CAGACAGTTAAATCACTCAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
DB CAGACAGTTAAATCACTCAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3059
2821 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 3000
DB AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 3119
2940 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 3060
DB AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 3179
2881 AAGGAACCTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAAT 2940
DB AAGGAACCTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAAT 3059
3000 AAGGAACCTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAAT 2941
DB AAGGAACCTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAAT 3060
3060 CCACCACTTTTCCCACTCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAGAG 3001
DB CCACCACTTTTCCCACTCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAGAG 3120
3001 GAAACCTTTGAGGAACATTCATGTCACCTGAAGAGAAATGGGAATGGAACATTCCTCA 3120
DB GAAACCTTTGAGGAACATTCATGTCACCTGAAGAGAAATGGGAATGGAACATTCCTCA

3061 AGTACAGTGCACCAATTTAGCGGTAAATAACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3120
DB AGTACAGTGCACCAATTTAGCGGTAAATAACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3239
3121 TCAACGCAATATTAATGAAGTAGGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3180
DB TCAACGCAATATTAATGAAGTAGGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3299
3240 TCAACGCAATATTAATGAAGTAGGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3240
DB TCAACGCAATATTAATGAAGTAGGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3359
3181 ATAGGTTCCAGTGTAGAAACATTTCAAGCAGAACTTAGTGAAGAGGCGCCAAATG 3300
DB ATAGGTTCCAGTGTAGAAACATTTCAAGCAGAACTTAGTGAAGAGGCGCCAAATG 3419
3241 AATGCTATGCTTAGAATAGGGTTCGAACTCAGGCTCTATAACAAAGTCTTCTCTGGA 3360
DB AATGCTATGCTTAGAATAGGGTTCGAACTCAGGCTCTATAACAAAGTCTTCTCTGGA 3479
3301 AGTAATGTAGATCTCTGAAATAAAGCAAGTAATGAAGAGTAGTTCAGACTGT 3420
DB AGTAATGTAGATCTCTGAAATAAAGCAAGTAATGAAGAGTAGTTCAGACTGT 3539
3420 AATACAGATTTCTCTCAATCTGATTTTCAAGTATTTAGAACAGCTTATGGAGTAGT 3480
DB AATACAGATTTCTCTCAATCTGATTTTCAAGTATTTAGAACAGCTTATGGAGTAGT 3599
3421 CATGCAATCTCAGGTTTGTCTGAGACACCTCATGACCTGTGTAGATGATGGTGAATAAG 3540
DB CATGCAATCTCAGGTTTGTCTGAGACACCTCATGACCTGTGTAGATGATGGTGAATAAG 3660
3481 GAGAGATCTAGTTTGTCTGAAATGACATTAAGGAAGTCTGCTGTTTGTAGCAAAAGC 3600
DB GAGAGATCTAGTTTGTCTGAAATGACATTAAGGAAGTCTGCTGTTTGTAGCAAAAGC 3720
3600 GAGAGATCTAGTTTGTCTGAAATGACATTAAGGAAGTCTGCTGTTTGTAGCAAAAGC 3780
DB GAGAGATCTAGTTTGTCTGAAATGACATTAAGGAAGTCTGCTGTTTGTAGCAAAAGC 3839
3661 GAAGAGCTTCTCTGCTTCCACACCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3721
DB GAAGAGCTTCTCTGCTTCCACACCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3840
3780 GAAGAGCTTCTCTGCTTCCACACCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3840
DB GAAGAGCTTCTCTGCTTCCACACCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3959
3721 TCTACTAGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGGAATTTA 3900
DB TCTACTAGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGGAATTTA 4019
3840 TCTACTAGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGGAATTTA 3960
DB TCTACTAGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGGAATTTA 4079
3781 TTATCATTTGAAGATAGCTTAAATGACCTGAGTAAACAGGTAATTTGGCAAGGCACTCT 3961
DB TTATCATTTGAAGATAGCTTAAATGACCTGAGTAAACAGGTAATTTGGCAAGGCACTCT 4080
3900 TTATCATTTGAAGATAGCTTAAATGACCTGAGTAAACAGGTAATTTGGCAAGGCACTCT 3900
DB TTATCATTTGAAGATAGCTTAAATGACCTGAGTAAACAGGTAATTTGGCAAGGCACTCT 4020
3841 CAGGAACATCACCTTTAGTGAGGAAACAAATGTTTCTGCTAGCTGTTTCTTTCACAGTGC 3960
DB CAGGAACATCACCTTTAGTGAGGAAACAAATGTTTCTGCTAGCTGTTTCTTTCACAGTGC 3960
3901 AGTGAAATGGAGAGCTTCACTGCAATTAACAAACCCAGGATCTTCTGCTGATGTTCT 4079
DB AGTGAAATGGAGAGCTTCACTGCAATTAACAAACCCAGGATCTTCTGCTGATGTTCT 4020
4020 AGTGAAATGGAGAGCTTCACTGCAATTAACAAACCCAGGATCTTCTGCTGATGTTCT 4020
DB AGTGAAATGGAGAGCTTCACTGCAATTAACAAACCCAGGATCTTCTGCTGATGTTCT 4020
3961 TCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTGGTCTGAGTGAACAAGGAATG 4080
DB TCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTGGTCTGAGTGAACAAGGAATG 4080
4021 GTTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGTAATTAATCAAGAGAGCAAGC 4199
DB GTTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGTAATTAATCAAGAGAGCAAGC 4140
4140 GTTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGTAATTAATCAAGAGAGCAAGC 4140
DB GTTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGTAATTAATCAAGAGAGCAAGC 4259
4081 ATGGAATTCAAACTTAGGTGAAGCAGTCTGAGTGTGAGTGAAGCAAGGCTCTCTGAA 4200
DB ATGGAATTCAAACTTAGGTGAAGCAGTCTGAGTGTGAGTGAAGCAAGGCTCTCTGAA 4141
4200 ATGGAATTCAAACTTAGGTGAAGCAGTCTGAGTGTGAGTGAAGCAAGGCTCTCTGAA 4200
DB ATGGAATTCAAACTTAGGTGAAGCAGTCTGAGTGTGAGTGAAGCAAGGCTCTCTGAA

Db	4260	GA	CTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCATCAGCAGAGGENTACCATG	4319
Qy	4201	CA	ACATAAACCCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAACTGTGTAGAACAG	4260
Db	4320	CA	ACATAAACCCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAACTGTGTAGAACAG	4379
Qy	4261	CA	TGGGAGCGACGCTTCTTAAACAGCTACCCCTTCCATCATATAGTGAAGTCTTCTGCCCCTGAG	4320
Db	4380	CA	TGGGAGCGACGCTTCTTAAACAGCTACCCCTTCCATCATATAGTGAAGTCTTCTGCCCCTGAG	4439
Qy	4321	GA	CTTGGGAAATCCAGAAACAAGACACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGT	4380
Db	4440	GA	CTTGGGAAATCCAGAAACAAGACACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGT	4499
Qy	4381	AG	TGAATACCCCTATAGCCAGAAATCCAGAACGCTTTTCTGCTGACAAGTTTGAGGTGCT	4440
Db	4500	AG	TGAATACCCCTATAGCCAGAAATCCAGAACGCTTTTCTGCTGACAAGTTTGAGGTGCT	4559
Qy	4441	GC	AGATAGTTTCTACCAAGTAAAAATAAAGAACACAGAGTGGAAAAAGTCAATCCCTTCTTAAA	4500
Db	4560	GC	AGATAGTTTCTACCAAGTAAAAATAAAGAACACAGAGTGGAAAAAGTCAATCCCTTCTTAAA	4619
Qy	4501	TG	CCCATCATATAGATGATAGTGGTGATCATNGCACAGTTGCTCTGCGAGTCTTTCAGAAATAGA	4560
Db	4620	TG	CCCATCATATAGATGATAGTGGTGATCATNGCACAGTTGCTCTGCGAGTCTTTCAGAAATAGA	4679
Qy	4561	AA	CTACCATCTCTCAAGAGGAGCTCATTTAAAGTCTTCTGATGTGAGGAGGACAAAGCTGGAA	4620
Db	4680	AA	CTACCATCTCTCAAGAGGAGCTCATTTAAAGTCTTCTGATGTGAGGAGGACAAAGCTGGAA	4739
Qy	4621	GAG	TCTGGGCCACACGATTTTGAACGGAAACATCTTATTTGCCAAGCGCAAGATCTTAGAGGGA	4680
Db	4740	GAG	TCTGGGCCACACGATTTTGAACGGAAACATCTTATTTGCCAAGCGCAAGATCTTAGAGGGA	4799
Qy	4681	AC	CCCTTACCTTGGATCTGGAAATCAGCGCTCTTCTCTGATGACCGCTGAAATCTGATCTT	4740
Db	4800	AC	CCCTTACCTTGGATCTGGAAATCAGCGCTCTTCTCTGATGACCGCTGAAATCTGATCTT	4859
Qy	4741	GA	AGACAGAGCCCCAGAGTCAGCTCTGTTTGGCAACATACCATCTTCAACCTCTGCAATG	4800
Db	4860	GA	AGACAGAGCCCCAGAGTCAGCTCTGTTTGGCAACATACCATCTTCAACCTCTGCAATG	4919
Qy	4801	AA	AGTTCCCATNTTGAAGTTGCAGAAATCTGCCCAGGGTCCAGCTGCTGCTCATACTCT	4860
Db	4920	AA	AGTTCCCATNTTGAAGTTGCAGAAATCTGCCCAGGGTCCAGCTGCTGCTCATACTCT	4979
Qy	4861	GAT	ACTCTCTGGGTATATGCAATGGAGAAAGTGTGACGAGGAGAGGACCGCAATTTGACA	4920
Db	4980	GAT	ACTCTCTGGGTATATGCAATGGAGAAAGTGTGACGAGGAGAGGACCGCAATTTGACA	5039
Qy	4921	GCT	TCAACAGAAAGGGTCAACAAAAGAAATGTCATGCTGGTGTCTGGCTGACCCCGAA	4980
Db	5040	GCT	TCAACAGAAAGGGTCAACAAAAGAAATGTCATGCTGGTGTCTGGCTGACCCCGAA	5099
Qy	4981	GA	ATTTATGCTCGTGTACAGTTTGCAGAAACACACATCATCTTTAACTTAATCTTAAT	5040
Db	5100	GA	ATTTATGCTCGTGTACAGTTTGCAGAAACACACATCATCTTTAACTTAATCTTAAT	5159
Qy	5041	ACT	GAAGAGACTACTCATGTTGTTTATGAAACACAGATGCTGAGTTTCTGTTGTGCAACGGACA	5100
Db	5160	ACT	GAAGAGACTACTCATGTTGTTTATGAAACACAGATGCTGAGTTTCTGTTGTGCAACGGACA	5219
Qy	5101	CT	GAATATTTTCTAGGAATTGGCGAGGAAATATGGGTAGTTAGCTATTTCTGGGTGACC	5160
Db	5220	CT	GAATATTTTCTAGGAATTGGCGAGGAAATATGGGTAGTTAGCTATTTCTGGGTGACC	5279
Qy	5161	CAG	TCTATTAAAGAAAGAAATAATGCTGAATGAGCATGATTTTGAATCAGAGGAGATGTG	5220
Db	5280	CAG	TCTATTAAAGAAAGAAATAATGCTGAATGAGCATGATTTTGAATCAGAGGAGATGTG	5339
Qy	5221	GT	CAATGGAGAAACCAACAAAGTCCAAAGCGAGCAGAGAAATCCGACGACAGAAAGATC	5280

is useful for: (a) identifying individuals having BRCA1 gene mutations and having an increased susceptibility to breast or ovarian cancer, or identifying a mutation that increases the genetic susceptibility to breast or ovarian cancer; (b) avoiding misinterpretation of polymorphisms found in the BRCA1 gene; (c) determining the presence of a previously unknown mutation in the BRCA1 gene; (d) probing a human sample of the BRCA1 gene by allele to determine the presence of either polymorphic alleles or mutations; and (e) performing diagnosis with a reagent derived from the BRCA1 (omil) cDNA sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene, which are used in an example from the present invention

SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5589; DB 3; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTATCTGCTCTTCGCTTGAAGAGTACAAAATGTCATTAACTCTATGCGAGAA 60
 DB 120 ATGGATTATCTGCTCTTCGCTTGAAGAGTACAAAATGTCATTAACTCTATGCGAGAA 179

QY 61 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGAC 120
 DB 180 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGAC 239

QY 121 CACATATTTTGGAAATTTTGGATGCTGAAACTTCTCAACAGAGAAAGGGCTTTCACAG 180
 DB 240 CACATATTTTGGAAATTTTGGATGCTGAAACTTCTCAACAGAGAAAGGGCTTTCACAG 299

QY 181 TGTCTTTATGTAAGATCATATAACCAAGAGGCTTACAGAAAGTACGAGATTAGT 240
 DB 300 TGTCTTTATGTAAGATCATATAACCAAGAGGCTTACAGAAAGTACGAGATTAGT 359

QY 241 CAACTTGTGAGAGCTATTTGAAATCAATTTGTGCTTTTTCAGCTTTCACACAGTTTGGAG 300
 DB 360 CAACTTGTGAGAGCTATTTGAAATCAATTTGTGCTTTTTCAGCTTTCACACAGTTTGGAG 419

QY 301 TATGCAACAGCTATTAATTTTCCAAAGAGGAAATTAATCTCTGCAACATCTAAAGAT 360
 DB 420 TATGCAACAGCTATTAATTTTCCAAAGAGGAAATTAATCTCTCTGAAACATCTAAAGAT 479

QY 361 GAAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT 420
 DB 480 GAAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT 539

QY 421 GAAACCGGAAATCTTCTTCGAGGAAACCGAGTCTCAGTGTCCAACTCTCTAAACCTTGGG 480
 DB 540 GAAACCGGAAATCTTCTTCGAGGAAACCGAGTCTCAGTGTCCAACTCTCTAAACCTTGGG 599

QY 481 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTCTGTCTACATT 540
 DB 600 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTCTGTCTACATT 659

QY 541 GAAATTTGGAGTCTGATTTCTTGAAGATACCGTTTAAAGGCAACTTATTCAGTGTGGGA 600
 DB 660 GAAATTTGGAGTCTGATTTCTTGAAGATACCGTTTAAAGGCAACTTATTCAGTGTGGGA 719

QY 601 GATCAAGAAATTTTACAAATCACCCCTCAAGGACCGGGATGAATCAGTTTGGATTCT 660
 DB 720 GATCAAGAAATTTTACAAATCACCCCTCAAGGACCGGGATGAATCAGTTTGGATTCT 779

QY 661 GCAAAAAGGCTGTGTGGAATTTTCTGAGACGATGTAAACAAATCTGAAACATCATCAA 720
 DB 780 GCAAAAAGGCTGTGTGGAATTTTCTGAGACGATGTAAACAAATCTGAAACATCATCAA 839

QY 721 CCCAGTAAATATGATTTGAAACCACTGAGAGGCTGAGCTGAGAGGCTCCAGAAAG 780
 DB 840 CCCAGTAAATATGATTTGAAACCACTGAGAGGCTGAGCTGAGAGGCTCCAGAAAG 899

QY 781 TATCAGGGTATTTCTGTTTCAAACTTGTGATGTGGAGCCATGTGGCAACAAATCTCATGCC 840
 DB 900 TATCAGGGTATTTCTGTTTCAAACTTGTGATGTGGAGCCATGTGGCAACAAATCTCATGCC 959

QY 841 AGCTCATTTACAGCTAGAGACAGCAGTTTATTACTTCACTAAAGACAGAAATGAATGTAGAA 900
 DB 960 AGCTCATTTACAGCTAGAGACAGCAGTTTATTACTTCACTAAAGACAGAAATGAATGTAGAA 1019

QY 901 AAGGCTGAATTTCTGTAATTAAGACAAACAGCCTGCTTAGCAAGGAGCCAAACATACACA 960
 DB 1020 AAGGCTGAATTTCTGTAATTAAGACAAACAGCCTGCTTAGCAAGGAGCCAAACATACACA 1079

QY 961 TGGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTA 1020
 DB 1080 TGGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTA 1139

QY 1021 GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGCAATTAAGCAGAAATCTGCATGC 1080
 DB 1140 GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGCAATTAAGCAGAAATCTGCATGC 1199

QY 1081 TCAGAGAAATCTCTAGAGATATCTGAAGATGTTCTTTGGATTAACACATTAATAGCAGCAATTCCAG 1140
 DB 1200 TCAGAGAAATCTCTAGAGATATCTGAAGATGTTCTTTGGATTAACACATTAATAGCAGCAATTCCAG 1259

QY 1141 AAAGTTAATGATGTTGTTTCCAGAGTGAATGATGTTTGGATTAACACATTAATAGCAGCAATTCCAG 1200
 DB 1260 AAAGTTAATGATGTTGTTTCCAGAGTGAATGATGTTTGGATTAACACATTAATAGCAGCAATTCCAG 1319

QY 1201 GGGGAGTCTGAATCAAAATGCCCCAAGTAGCTGATGTTTGGACGTTTCTAAATAGAGGTAGAT 1260
 DB 1320 GGGGAGTCTGAATCAAAATGCCCCAAGTAGCTGATGTTTGGACGTTTCTAAATAGAGGTAGAT 1379

QY 1261 GAATATTTCTGTTCTTCCAGAGAAATAGACTTACTTGGCCAGTGAATCTCTCATGAGGCTTTTA 1320
 DB 1380 GAATATTTCTGTTCTTCCAGAGAAATAGACTTACTTGGCCAGTGAATCTCTCATGAGGCTTTTA 1439

QY 1321 ATATGTTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAAATA 1380
 DB 1440 ATATGTTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAAATA 1499

QY 1381 TTTGGGAAACCTATCGAAGAGAGGAGGCTTCCCAACTTAAGCCATGTAACCTGAGAAAT 1440
 DB 1500 TTTGGGAAACCTATCGAAGAGAGGAGGCTTCCCAACTTAAGCCATGTAACCTGAGAAAT 1559

QY 1441 CTAATTTAGAGCAATTTGTTTACTTGAGCCACAGATAATACAGAGGCTTCCCTCACAATA 1500
 DB 1560 CTAATTTAGAGCAATTTGTTTACTTGAGCCACAGATAATACAGAGGCTTCCCTCACAATA 1619

QY 1501 AAATTAAGCCTTAAGAGGAGCCTTACATCAGGCTTCACTGAGGATTTTATCAAGAAA 1560
 DB 1620 AAATTAAGCCTTAAGAGGAGCCTTACATCAGGCTTCACTGAGGATTTTATCAAGAAA 1679

QY 1561 GCAGATTTGCGAGTTCAAAAGAGCTTCTGAAATGATTAATCAGGAACTACCAAAACGAG 1620
 DB 1680 GCAGATTTGCGAGTTCAAAAGAGCTTCTGAAATGATTAATCAGGAACTACCAAAACGAG 1739

QY 1621 CAGAAATGCTCAAGTGTGATTAATTTACTTAATGTTGTCATGAGAAATAAAAAAGAGGTGAT 1680
 DB 1740 CAGAAATGCTCAAGTGTGATTAATTTACTTAATGTTGTCATGAGAAATAAAAAAGAGGTGAT 1799

QY 1681 TCTATTTCAAGATGAGAAATTTCTTAACCCATAGATCACTCGAAAAGAGATCTGCTTTC 1740
 DB 1800 TCTATTTCAAGATGAGAAATTTCTTAACCCATAGATCACTCGAAAAGAGATCTGCTTTC 1859

QY 1741 AAAACGAAAGCTGAACTATTAAGCAGCAGTATTAAGCAATATGAACTCGAAATTAATATC 1800
 DB 1860 AAAACGAAAGCTGAACTATTAAGCAGCAGTATTAAGCAATATGAACTCGAAATTAATATC 1919

QY 1801 CACAAATTCAAAAGCACTTAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATT 1860
 DB 1920 CACAAATTCAAAAGCACTTAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATT 1979

QY 1861 CATGCGCTTGAACCTAGTGTAGTAAATCTAAGCCACCTAATGTTCTGTAATTTGCAA 1920
 DB 1980 CATGCGCTTGAACCTAGTGTAGTAAATCTAAGCCACCTAATGTTCTGTAATTTGCAA 2039

1921 ATTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTC 1980
1922 GAAAACTTTCAGGAAACATTCATCTGCTCACTGAAAGAAATGGGAATGAGAACTTCCA 3179
2040 ATTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTC 2099
1981 AGGCAAGCAGAGAAACCTACAACTCATGGAAGTGAAGAACCTGGAACCTGAGCCAGAG 2040
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2520 TGTTGAGTCACTGTGAGCACTTCCAAACCCCAAGGCACTAACTCATGTTGTTCCAAA 2579
2461 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGT 2520
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2881 AACGAACTGGACTCATTAATCAAAATAAATCAAGCACTTTTACAAAACCCATATCGTATA 2940
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3180 AGTACAGTGAAGCAAAATGAGCGTAAATAACAATTAGAGAAATGTTTTTAAAGGAGCCAGC 3239
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3900 TTATCATTTGAAGAAATAGCTTAAATGACTGCAAGTAAACAGTATATTTGGCAAGGCATCT 3959
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4140 GTTTCAGATGATGAAGAAAG 4199
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Db	5340	GTCAATGGAGAGAAACCCAAAGGTCCAAAGCGAGCAAGAGAAATCCCAAGGACAGAAAGATC	5399
Qy	5281	TTCAAGGGGGCTAGAAATCTGTGCTATGGGCCCTTTACCAACATGCCACAGAGATCAACTG	5340
Db	5400	TTCAAGGGGGCTAGAAATCTGTGCTATGGGCCCTTTACCAACATGCCACAGAGATCAACTG	5459
Qy	5341	GAATGGATGGTACACGCTGTGTGTGCTTCTGTGGTGGAGAGCTTTTCATCAATTCACCCCTT	5400
Db	5460	GAATGGATGGTACACGCTGTGTGTGCTTCTGTGGTGGAGAGAGCTTTTCATCAATTCACCCCTT	5519
Qy	5401	GGCACAGGCTGTCCACCCCAATTTGTTGTGTCAGCCAGATGCCCTGGACAGAGGACAATGGC	5460
Db	5520	GGCACAGGCTGTCCACCCCAATTTGTTGTGTCAGCCAGATGCCCTGGACAGAGGACAATGGC	5579
Qy	5461	TTCCATGCAATTTGGGCGAGATGTGTGAGGCACTGTGTGGTGAACCCGAGAGTGGGTGTTGGAC	5520
Db	5580	TTCCATGCAATTTGGGCGAGATGTGTGAGGCACTGTGTGGTGAACCCGAGAGTGGGTGTTGGAC	5639
Qy	5521	AGTGTAGCACTTACACAGTCCAGGAGCTGGACACCTACTCTGATACCCAGATCCCCCAC	5580
Db	5640	AGTGTAGCACTTACACAGTCCAGGAGCTGGACACCTACTCTGATACCCAGATCCCCCAC	5699
Qy	5581	AGCCACTAC 5589	
Db	5700	AGCCACTAC 5708	
RESULT 3			
ACA61333			
ID	ACA61333 standard; cDNA; 5711 BP.		
XX			
AC	ACA61333;		
AC			
DT	07-AUG-2003 (first entry)		
XX			
DS	Human BRCA1 allele omi2, cDNA.		
XX			
KW	Human; ss; gene; BRCA1; omi2; gene therapy; tumour; breast cancer;		
KW	ovarian cancer; prostate cancer; colon cancer; SNP;		
KW	single nucleotide polymorphism.		
XX			
XX	Homo sapiens.		
XX			
PH	Key		
FT	CDS		
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PN	US2003022184-A1.		

30-JAN-2003.

22-OCT-2001; 2001US-00982828.

12-FEB-1996; 96US-00598591.

12-FEB-1997; 97US-00798691.

06-MAY-1998; 98US-00074453.

(ONCO-) ONCORMED INC.

Murphy PD., Allen ACP, Alvares CP, Critz BS, Olson SJ, Thurber D; Zeng B;

WPI; 2003-456286/43.

P-PSDB; ABU61604.

New protein sequence comprising an amino acid sequence derived from the BRCA1 omi1, omi2 or omi3 sequence useful in performing gene therapy for treating patients suspected of having tumor, e.g. breast, ovarian, prostate or colon cancer.

Claim 5; Page 25-28; 60pp; English.

The invention relates to a protein sequence comprising an amino acid sequence derived from the human BRCA1 omi1, omi2 or omi3 sequences appearing as ABU61603 ABU61605. Also included are determining the consensus genomic sequence or consensus coding sequence for a target gene, oligonucleotide probes (each capable of hybridizing to a sample BRCA1 omi gene/cDNA appearing as AC61332-AC61334) or their complements, a chip array having elements for performing allele specific sequence-based techniques comprising a solid phase chip and oligonucleotides having n different nucleotide sequences (where n is an integer greater than or equal to 7, where the oligonucleotides are bound to the solid phase chip in a manner that permits the oligonucleotides to effectively hybridize to complementary oligonucleotides or polynucleotides, and the oligonucleotides having different nucleotide sequence are bound to the solid phase chip at different locations so that a particular location on the solid phase chip exclusively binds oligonucleotides having a specific nucleotide sequence, and the oligonucleotides are capable of specifically hybridizing to the BRCA1 omi DNA), performing gene therapy on a patient, treating a patient suspected of having a tumor, a expression/cloning vector comprising the BRCA1 DNA sequence (or fragments), preventing the formation or growth of a tumor, a host cell transformed with the vector and an anti-BRCA1 antibody. The protein sequences are useful in performing gene therapy for treating patients suspected of having a tumor, e.g. breast cancer, ovarian cancer, prostate cancer or colon cancer. The antibody is useful as an immunogen. The present sequence is a cDNA representing the omi2 allele of the BRCA1 gene

Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5589; DB 8; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCATTATGCTATGTCAGAAA 60

120 ATGGATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCATTATGCTATGTCAGAAA 179

61 ATCTTAGAGTGTCCATCTGCTGAGGTGATCAAGGAACCTGCTCCACAAAGTGTGAC 120

180 ATCTTAGAGTGTCCATCTGCTGAGGTGATCAAGGAACCTGCTCCACAAAGTGTGAC 239

121 CACATATTTTGCAGAAATTTGCATGCTGAACTTCTCAACAGAAAGAGGCGCTTCACAG 180

240 CACATATTTTGCAGAAATTTGCATGCTGAACTTCTCAACAGAAAGAGGCGCTTCACAG 299

181 TGTCTTTATGTAGATGATATATACCAAGAGGAGCTTACAGAAAGTACAGATTAGT 240

300 TGTCTTTATGTAGATGATATATACCAAGAGGAGCTTACAGAAAGTACAGATTAGT 359

241 CAACTTGTGAGAGCTATTGAAATCATTTTGTGCTTTTCAGCTTGTGACACAGGTTGGAG 300

Db 360 CAACCTTGTGAGAGCTATTGAAATCATTTTGTGCTTTTCAGCTTGTGACACAGGTTTGGAG 419

Qy 301 TATGCAAAACAGCTATATATTTTGCAGAAAGAGGAAAAATAACTCTCTCTGAACATCTAAAAGAT 360

Db 420 TATGCAAAACAGCTATATATTTTGCAGAAAGAGGAAAAATAACTCTCTCTGAACATCTAAAAGAT 479

Qy 361 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGGCCAAAGACATCTTACAGAGT 420

Db 480 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGGCCAAAGACATCTTACAGAGT 539

Qy 421 GAACCCGAAAATCTCTCTTTCAGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGGGA 480

Db 540 GAACCCGAAAATCTCTCTTTCAGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGGGA 599

Qy 481 ACTGTGAGAACTCTGAGGACAAAGACGCGGATCAACCTCAAAAGAGCTGTGTCTACATT 540

Db 600 ACTGTGAGAACTCTGAGGACAAAGACGCGGATCAACCTCAAAAGAGCTGTGTCTACATT 659

Qy 541 GAATTTGGGATCTGATTTCTCTGAAGATACCGTTTAATAAGGCACTTATTTCAGTGTGGGA 600

Db 660 GAATTTGGGATCTGATTTCTCTGAAGATACCGTTTAATAAGGCACTTATTTCAGTGTGGGA 719

Qy 601 GATCAGAAATGTTTACAAATCACCCCTCAAGGAAACCAAGGATGAAATCAGTTTGGATTCT 660

Db 720 GATCAGAAATGTTTACAAATCACCCCTCAAGGAAACCAAGGATGAAATCAGTTTGGATTCT 779

Qy 661 GCAGAAAGGCTCTGTTGTAATTTCTGAGACGCGATGTAACAAATCTGAGACATCTCAA 720

Db 780 GCAGAAAGGCTCTGTTGTAATTTCTGAGACGCGATGTAACAAATCTGAGACATCTCAA 839

Qy 721 CCAGTAATAATGATTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAAG 780

Db 840 CCAGTAATAATGATTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAAG 839

Qy 781 TATCAGGAGTGTCTGTTTCAAACTGCTGAGGCGCATGTTGGCAAAATCTCATGCC 840

Db 900 TATCAGGAGTGTCTGTTTCAAACTGCTGAGGCGCATGTTGGCAAAATCTCATGCC 959

Qy 841 AGCTCATTACAGCATGAGAACAGCAGTTTATTACTCATAAAGACAGAAATGATGTAGAA 900

Db 960 AGCTCATTACAGCATGAGAACAGCAGTTTATTACTCATAAAGACAGAAATGATGTAGAA 1019

Qy 901 AAGCTGTAATCTGTAATAAAGCAAAAGCCCTGCTTGAAGAGGCAAAATACACAGA 960

Db 1020 AAGCTGTAATCTGTAATAAAGCAAAAGCCCTGCTTGAAGAGGCAAAATACACAGA 1079

Qy 961 TGGGCTGGAGTAAGGAAACATGTAATGATAGCGGACTCCAGACACAGAAAAGGTA 1020

Db 1080 TGGGCTGGAGTAAGGAAACATGTAATGATAGCGGACTCCAGACACAGAAAAGGTA 1139

Qy 1021 GATCTGAATGCTGATCCCTGTTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGC 1080

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Db 1200 TCAGAGAACTCTAGAGATACGAGGATGTTCTTGGATACCACTAAATAGCAGCATTCAG 1259

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Db 1260 AAAGTTAATAGAGTGGTGTTCAGAGAAAGTGAATGTAAGCTGTGTAGGTTCTGATGACTCAGAT 1319

Qy 1201 GGGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTATGGAAGTCTTAATAGAGTAGAT 1260

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Db 1920 CACAAATCAAAGACCTCAAAGAAATAGGCTGAGGAGGAGTCTCTACAGGACATATT 1979
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QY 3361 AATPACAGATTTCTCCATATCTGATTTTCAAGTTCAGTAACTTAGAACAGCCTTAGGAAAGTAGT 3420
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QY 3481 GAAGATACAGTTTCTCTGAAATGACATTTAAGGAAAGTTCGCTGCTTTTACGAAAGC 3540
Db 3600 GAAGATACAGTTTCTCTGAAATGACATTTAAGGAAAGTTCGCTGCTTTTACGAAAGC 3659

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Qy	3781	TTATCAATTTGAAAGATPAGCTTTAAATGATGCGAGTAAACGAGTAAATATTGGCCAAAGCATCT	3840	
Db	3900	TTATCAATTTGAAAGATPAGCTTTAAATGATGCGAGTAAACGAGTAAATATTGGCCAAAGCATCT	3959	
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Db	4020	AGTGAATTTGGAAGACTTGACTGCAATACAAACA	CCCAAGATCCTTTCTGATTTGGTTCT	4079
Qy	3961	TCCAAACAAATGAGGCATAGTCTGAAGCCAGGAGTTGGTCTGAGTGACAGGAATTG	4020	
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Db	4260	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAA	CCCTCAGCAGAGGATACCATG	4319
Qy	4201	CAACATAACCTGATAAGCTCCAGCAGGAATGCTGAACTAGAGCTGTGTAGAACAG	4260	
Db	4320	CAACATAACCTGATAAGCTCCAGCAGGAATGCTGAACTAGAGCTGTGTAGAACAG	4379	
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Qy	4321	GACCTGGGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCCACAGAAAAGT	4380	
Db	4440	GACCTGGGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCCACAGAAAAGT	4499	
Qy	4381	AGTGAATACCTATTAAGCCGAATCCAGAGGCGCTTCTGCTGACAGTTTGGGTGTCT	4440	
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5461	QY		TTCCATGCAATTTGGGAGATGTGTGAGGCAACCTGTGGTACCCGAGAGTGGGTGTGGAC	5520
5580	DB		TTCCATGCAATTTGGGAGATGTGTGAGGCAACCTGTGGTACCCGAGAGTGGGTGTGGAC	5639
5521	QY		AGTGTAGCACTCTACAGTGCACAGGAGCTGGACACCTTACTGATACCCAGATCCCCCCAC	5580
5640	DB		AGTGTAGCACTCTACAGTGCACAGGAGCTGGACACCTTACTGATACCCAGATCCCCCCAC	5699
5581	QY		AGCCACTAC 5589	
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RESULT 4
ADC63291
ID ADC63291 standard; cDNA; 5711 BP.
XX
AC ADC63291;

[illegible]

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RESULT 5
AAV46468
ID AAV46468 standard; cDNA; 5711 BP.

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XX AAV46468;
AC
XX
XX 18-NOV-1998 (first entry)
XX
XX Human BRCA1 omi3 polymorphism #4 cDNA.
XX
XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
XX
XX Homo sapiens.
XX
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XX /product= "BRCA1 omi3 protein"
XX 3232
XX variation
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XX 12-MAY-1998.
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XX 12-FEB-1997; 97US-00798691.
XX
XX 12-FEB-1996; 96US-00598591.
XX
XX (ONCO-) ONCORMED INC.
XX
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
XX Critz BS;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.
XX
XX Claim 2e; Page; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi3 gene in which a polymorphic variation occurs at
XX nucleotide 3232. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer. The
XX sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome 17q
XX which is known to be linked to cancer susceptibility, especially breast
XX cancer. Cells containing a mutation in this gene lose the wild-type
XX function of BRCA1 and are more susceptible to cancers. NOTE: This
XX sequence does not appear in the specification but has been created from
XX the wild type BRCA1 omi3 gene represented in AAV46450
XX
XX Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;
XX
XX Query Match 100.0%; Score 5588.6; DB 2; Length 5711;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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XX
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XX
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```

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Qy 1361 GAATATCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGTACTCTCATGAGGCTTTA 1320
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Qy 1381 TTTCGGAAACCTATCGGAAGAGCGCAAGCTCCCAACTTTAGCCATGTAATCTGAAAT 1440
Db 1500 TTTCGGAAACCTATCGGAAGAGCGCAAGCTCCCAACTTTAGCCATGTAATCTGAAAT 1559
Qy 1441 CTAATATAGAGCAATTTGTTACTTGAGCCACAGATATACAGAGCGTCCCTCACAAAT 1500
Db 1560 CTAATATAGAGCAATTTGTTACTTGAGCCACAGATATACAGAGCGTCCCTCACAAAT 1619
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Db 1680 GCAGATTTGCGAGTTCAAGACACTCTGAATGATTAATCAGGAACTAACCAACGAG 1739
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Qy 1741 AAPACGAAGCTGAACCTATAAGCAGCAGTATAGCAATATGGAATCTGAATTAATATC 1800
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 RESULT 6
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 XX 18-NOV-1998 (first entry)
 XX Human BRCA1 omi3 polymorphism #1 cDNA.
 XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 XX chromosome 17q; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
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 XX /product= "BRCA1 omi3 protein"
 XX variation 2201
 XX /tag= b
 XX /note= "This polymorphic variation can be a C or T
 XX nucleotide"
 XX US5750400-A.
 XX 12-MAY-1998.
 XX 12-FEB-1997; 97US-00798691.
 XX 12-FEB-1996; 96US-00598591.
 XX (ONCO-) ONCORMED INC.
 XX Olson SJ, Murphy PB, Zeng B, Alvarez CP, Schelter DB, Allen AC;
 XX Critz BS;
 XX WPI; 1998-296774/26.
 XX BRCA1 omi gene coding sequences - useful for distinguishing between
 XX polymorphisms and mutation(s) in the screening for disposition to breast
 XX or ovarian cancer.
 XX Claim 2e; Page; 54pp; English.
 XX This sequence encodes a human BRCA1 (breast and ovarian cancer
 XX predisposing gene) omi3 gene in which a polymorphic variation occurs at
 XX nucleotide 2201. This sequence and other polymorphic variations of this
 XX sequence are useful for the identification of an individual who may or
 XX may not have an increased susceptibility to breast or ovarian cancer. The
 XX sequences used identify gene changes which are due to polymorphisms,
 XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 XX suppressor) which is involved in genetic inheritance of cancers,
 XX especially breast and ovarian cancer. It is found at human chromosome 17q
 XX which is known to be linked to cancer susceptibility, especially breast
 XX cancer. Cells containing a mutation in this gene lose the wild-type
 XX function of BRCA1 and are more susceptible to cancers. NOTE: This
 XX sequence does not appear in the specification but has been created from
 XX the wild type BRCA1 omi3 gene represented in AAV46450
 XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;
 Query Match 100.0%; Score 5588.6; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 Db 120 ATGGATTATCTGCTCTTGGGTTGAAGAGTACAAAATGTCATTATGCTATGCGAAA 179
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 Db 180 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCCAAGTGTGAC 239
 QY 121 CACATATTTTGCATAATTTTGGCATCTGTAACCTTCTCAACGAGAGAAAGGGCTTCACAG 180
 Db 240 CACATATTTTGCATAATTTTGGCATCTGTAACCTTCTCAACGAGAGAAAGGGCTTCACAG 239
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 QY 241 CACATTTTGTGAGAGCTATTGAAAATCATTGTGCTTTTTCAGCTTGCACAGCTTTGGAG 300
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 QY 601 GATCAAGAAATGTTACAAATCACCCCTCAAGGAAACAGGGATGAATTCAGTTTGGATTCT 660
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1801 CACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATAT 1860
1920 CACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATAT 1979
1861 CATGCGCTTGAATCTAGTAGTCAAGTAAATCTAAGCCACCTAATTTGTACTGAATTCGAA 1920
1980 CATGCGCTTGAATCTAGTAGTCAAGTAAATCTAAGCCACCTAATTTGTACTGAATTCGAA 2039
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2040 ATTGATAGTGTCTTACAGTAGAGATAAAGAAATAAGTAAAGTAAAGTAAAGTAAAGTAA 2099
1981 AGGCACAGCAGACCTTACCACTCATGGAAGTAAAGAACTTGCATCTGAGGAGCCAGAG 2040
2100 AGGCACAGCAGACCTTACCACTCATGGAAGTAAAGAACTTGCATCTGAGGAGCCAGAG 2159
2041 AGTAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2100
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2220 AGTTAACAATGACCTGTTCTTTTACTTAAAGTGTCAATACCACTGAACTTAAAGAA 2279
2161 TTTGTCATCTAGCTTCCAG 2220
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2221 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTCGAAACT 2280

2340 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTCGAAACT 2399
2281 GAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTTGGTACTGATTTATGGCACTCAG 2340
2400 GAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTTGGTACTGATTTATGGCACTCAG 2459
2341 GAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTTGGTACTGATTTATGGCACTCAG 2400
2460 GAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTTGGTACTGATTTATGGCACTCAG 2519
2401 TGTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGAGACTAATTCATGGTGTTCGAAA 2460
2520 TGTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGAGACTAATTCATGGTGTTCGAAA 2579
2461 GAATATAGAAATGACACAGAGCGCTTTAAGTATCAATTCGGGACATGAAGTTAACCACTG 2520
2580 GAATATAGAAATGACACAGAGCGCTTTAAGTATCAATTCGGGACATGAAGTTAACCACTG 2639
2521 CCGGAAAACAGCATAGAAATGGAAGAAAGTGAACCTTGGTCTCAATTCAGGAAATGCGAAGAG 2580
2640 CCGGAAAACAGCATAGAAATGGAAGAAAGTGAACCTTGGTCTCAATTCAGGAAATGCGAAGAG 2699
2581 TTTCAAGTGTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAAGAG 2640
2700 TTTCAAGTGTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAAGAG 2759
2641 GAATGTCAACATCTCTGSCCACTCTGGTCTCTTAAAGAAAACAAAGTCCAAAAGTCACT 2700
2760 GAATGTCAACATCTCTGSCCACTCTGGTCTCTTAAAGAAAACAAAGTCCAAAAGTCACT 2819
2701 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGGCTGTAT 2760
2820 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGGCTGTAT 2879
2761 CAGACAGTGTAAATATCACTCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
2880 CAGACAGTGTAAATATCACTCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2939
2821 AATGCAAAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCTATCTATCTATCTATCTATCT 2880
2940 AATGCCAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCTATCTATCTATCTATCTATCTATCT 2999
2881 AACGAAAATGAGTCAATTTACTTCCAAATGAACATGACCTTTTACAAAACCCATATCTGTAT 2940
3000 AACGAAAATGAGTCAATTTACTTCCAAATGAACATGACCTTTTACAAAACCCATATCTGTAT 3059
2941 CCACCACTTTTCCCAATCAAGTCAATTTGTAAAACTTAAATGTAAAGAAAATCTGCTAGAG 3000
3060 CCACCACTTTTCCCAATCAAGTCAATTTGTAAAACTTAAATGTAAAGAAAATCTGCTAGAG 3119
3001 GAAAACTTTGAGGAACTTCAATGTCACTGAAAGAAATGCGGAAATGGAAGAACTTCCA 3060
3120 GAAAACTTTGAGGAACTTCAATGTCACTGAAAGAAATGCGGAAATGGAAGAACTTCCA 3179
3061 AGTACAGTGAAGCAATTTAGCCGTAAATCACTTACGAAATGTTTAAAGGAGCCAGC 3120
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3241 AATGCTATGCTTTAGATTAGGGGTTTTGCAACCTGAGGCTTATAAACAAGTCTTCTCTGGA 3300
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Qy 3361 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAAACAGCCCTATCGGAAGTAGT 3420
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Qy 3421 CATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAG 3480
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Qy 3481 GAAGATCTAGTTTGTCTGAAATAAGACATTAAGGAAAGTTCTGCTGTTTITAGCAAAAGC 3540
Db 3600 GAAGATCTAGTTTGTCTGAAATAAGACATTAAGGAAAGTTCTGCTGTTTITAGCAAAAGC 3659
Qy 3541 GTCCAGAGAGAGAGCTTAGCAGAGCTCTAGCCCTTTACCCATACACATTTTGGCTCAG 3600
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Db 3720 GGTTCACGAGAGGGGCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAGGAT 3779
Qy 3661 GAAGAGCTTCCCTGCTTCCACACTTGTATTTTGGTAAAGTAAACAATACTCTCTCAG 3720
Db 3780 GAAGAGCTTCCCTGCTTCCACACTTGTATTTTGGTAAAGTAAACAATACTCTCTCAG 3839
Qy 3721 TCTACTAGGATAGCACCGTTGCTACCGAGTGTCTGTTAAGAACACAGAGGAGAAATTA 3780
Db 3840 TCTACTAGGATAGCACCGTTGCTACCGAGTGTCTGTTAAGAACACAGAGGAGAAATTA 3899
Qy 3781 TTATCATTAAGATAGCTTAATGATCGATGAAACCGGTAATATTTGGGCAAGGAACTCT 3840
Db 3900 TTATCATTAAGATAGCTTAATGATCGATGAAACCGGTAATATTTGGGCAAGGAACTCT 3959
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Qy 3901 AGTGAAATGGGAAGCTTGATCGCAAAATACAAACACCGGAGATCTTCTGATGTTGTTCT 3960
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Qy 4381 AGTGAAATACCTTATAAGCCAGATTCACAGAGGCTTCTGCTGACAAAGTTTGGGTGCT 4440
Db 4500 AGTGAAATACCTTATAAGCCAGATTCACAGAGGCTTCTGCTGACAAAGTTTGGGTGCT 4559

Qy 4441 GCAGATAGTTCTACAGTAAATAAAGAACACAGGAGTGGAAAGTCTATCCCTCTTAAA 4500
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Qy 4681 ACCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCTGGAATCTGATCTTCT 4740
Db 4800 ACCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCTGGAATCTGATCTTCT 4859
Qy 4741 GAAGACAGAGCCCCACAGAGTCAAGTCTGTTGGCAACATACCACTTCAACCTCTGANTG 4800
Db 4860 GAAGACAGAGCCCCACAGAGTCAAGTCTGTTGGCAACATACCACTTCAACCTCTGANTG 4919
Qy 4801 AAGTTTCCCAATTTGAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4860
Db 4920 AAGTTTCCCAATTTGAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4979
Qy 4861 GATACCTGCTGGGTATANTGCATGGAGAAAGTGTGACGAGGAGGACGAGCAATGACA 4920
Db 4980 GATACCTGCTGGGTATANTGCATGGAGAAAGTGTGACGAGGAGGACGAGCAATGACA 5039
Qy 4921 GCTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTGAGACCCAGAA 4980
Db 5040 GCTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTGAGACCCAGAA 5099
Qy 4981 GAATTTATGCTGCTGATCAAGTTTGCAGAAACACACATCACTTTTAATCTAATTAAT 5040
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Qy 5161 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTC 5220
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Qy 5221 GTCAATGGAAGAAACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATC 5280
Db 5340 GTCAATGGAAGAAACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATC 5399
Qy 5281 TTCAAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACAAATGCTCCACAGATCAACTG 5340
Db 5400 TTCAAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACAAATGCTCCACAGATCAACTG 5459
Qy 5341 GAATGATGATGATCAGCTGTTGTTGCTTCTGTTGTTGAAGGAGCTTTTCACTTTCACCTT 5400
Db 5460 GAATGATGATGATCAGCTGTTGTTGCTTCTGTTGTTGAAGGAGCTTTTCACTTTCACCTT 5519
Qy 5401 GGCACAGGTTGTCACCAATTTGTTGTTGTCAGCAGATGCTGGACAGAGGACAAATGTC 5460
Db 5520 GGCACAGGTTGTCACCAATTTGTTGTTGTCAGCAGATGCTGGACAGAGGACAAATGTC 5579
Qy 5461 TTCCATGCAATTTGGGCAAGTGTGAGGACACCTGTTGTTGACCCGAGAGTGGGTGTTGGAC 5520
Db 5580 TTCCATGCAATTTGGGCAAGTGTGAGGACACCTGTTGTTGACCCGAGAGTGGGTGTTGGAC 5639

QY 5521 AGTGTAGCACTCTACCACTGCGAGAGCTGACACCTACCTGATACCCAGATCCCCAC 5580
 DB 5640 AGTGTAGCACTCTACCACTGCGAGAGCTGACACCTACCTGATACCCAGATCCCCAC 5699
 QY 5581 AGCCACTAC 5589
 DB 5700 AGCCACTAC 5708

RESULT 7

ID AAV46470 standard; cDNA; 5711 BP.
 XX AAV46470;

DT 18-NOV-1998 (first entry)

DE Human BRCA1 omi3 polymorphism #6 cDNA.

XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 KW chromosome 17q; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CD5 120-5711

FT /tag= a
 FT /product= "BRCA1 omi3 protein"

FT variation 4427

FT /tag= b

FT /note= "This polymorphic variation can be a T or C
 FT nucleotide"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-00798691.

XX 12-FEB-1996; 96US-00598591.

XX (ONCO-) ONCORMED INC.

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
 PI Critz BS;

XX WPI; 1998-296774/26.

XX BRCA1 omi gene coding sequences - useful for distinguishing between
 PT polymorphisms and mutation(s) in the screening for disposition to breast
 PT or ovarian cancer.

XX Claim 2e; Page; 54pp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer
 CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
 CC nucleotide 4427. This sequence and other polymorphic variations of this
 CC sequence are useful for the identification of an individual who may or
 CC may not have an increased susceptibility to breast or ovarian cancer. The
 CC sequences used identify gene changes which are due to polymorphisms,
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 CC suppressor) which is involved in genetic inheritance of cancers,
 CC especially breast and ovarian cancer. It is found at human chromosome 17q
 CC which is known to be linked to cancer susceptibility, especially breast
 CC cancer. Cells containing a mutation in this gene lose the wild-type
 CC function of BRCA1 and are more susceptible to cancers. NOTE: This
 CC sequence does not appear in the specification but has been created from
 CC the wild type BRCA1 omi3 gene represented in AAV46450

XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;

Query Match

100.0%; Score 5588.6; DB 2; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATCGATTATCTGCTCTCTGCGTTGAGAGAGTACAAATGCTATTATGCTATGTCAGAAA 60
 DB 120 ATGGAATTAATCTGCTCTCTGCGTTGAGAGAGTACAAATGCTATTATGCTATGTCAGAAA 179
 QY 61 ATCTTAGAGTCTCCATCTGCTGCGAGTTGATCAAGGAACCTGCTCCCAAAAGTGTGAC 120
 DB 180 ATCTTAGAGTCTCCATCTGCTGCGAGTTGATCAAGGAACCTGCTCCCAAAAGTGTGAC 239
 QY 121 CACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACGAGAGAAAGGCGCTTCACAG 180
 DB 240 CACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACGAGAGAAAGGCGCTTCACAG 299
 QY 181 TGTCTTTTATGTAAGAAATGATATAACCAAAAGGAGCTTCAAGAAAGTACGAGATTAGT 240
 DB 300 TGTCTTTTATGTAAGAAATGATATAACCAAAAGGAGCTTCAAGAAAGTACGAGATTAGT 359
 QY 241 CAACTTTTGAAGAGCTATTGAAATTCATTTGCTTTTCAGCTTTCACACAGGTTGGAG 300
 DB 360 CAACTTTTGAAGAGCTATTGAAATTCATTTGCTTTTCAGCTTTCACACAGGTTGGAG 419
 QY 301 TATGCAACAGCTATATATTTTGCATAAAAGGAGAAATTAATCTCTCTGAAACATCTTAAAGAT 360
 DB 420 TATGCAACAGCTATATATTTTGCATAAAAGGAGAAATTAATCTCTCTGAAACATCTTAAAGAT 479
 QY 361 GAAGTTTCTATGATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGT 420
 DB 480 GAAGTTTCTATCATTCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGT 539
 QY 421 GAAACCGGAAATTCCTTCTGAGGAGAAACCAAGTCTCAGTGTCCCACTCTTAACCTTGA 480
 DB 540 GAAACCGGAAATTCCTTCTGAGGAGAAACCAAGTCTCAGTGTCCCACTCTTAACCTTGA 599
 QY 481 ACTGTAGAACTCTGAGGACAAAGAGCGGATACAACTCTCAAAAGAGCTCTGTCTACATT 540
 DB 600 ACTGTAGAACTCTGAGGACAAAGAGCGGATACAACTCTCAAAAGAGCTCTGTCTACATT 659
 QY 541 GAATTGGGATCTGATTCTTCTGAAGATACCGTTTAAAGGCACTTTATGCACTGTGGGA 600
 DB 660 GAATTGGGATCTGATTCTTCTGAAGATACCGTTTAAAGGCACTTTATGCACTGTGGGA 719
 QY 601 GATCAAGAAATGTTACAAATCACTCTCAAGGAACCGGAGTGAATCACTAGTTTGAATTCT 660
 DB 720 GATCAAGAAATGTTACAAATCACTCTCAAGGAACCGGAGTGAATCACTAGTTTGAATTCT 779
 QY 661 GCAAAAAGCGCTCTTCTGAAATTTTCTGAGCGGATTAACAAATCTGAACTCATCAA 720
 DB 780 GCAAAAAGCGCTCTTCTGAAATTTTCTGAGCGGATTAACAAATCTGAACTCATCAA 839
 QY 721 CCCAGTAATAATGATTGTAACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAAG 780
 DB 840 CCCAGTAATAATGATTGTAACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAAG 899
 QY 781 TATCAGGTAATGTTCTGTTTCAAACTTGCATGGAGCGGATGCGGCAAAATCTCATGCC 840
 DB 900 TATCAGGTAATGTTCTGTTTCAAACTTGCATGGAGCGGATGCGGCAAAATCTCATGCC 959
 QY 841 AGCTCAATTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGACAGAAATGTAATGTAGAA 900
 DB 960 AGCTCAATTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGACAGAAATGTAATGTAGAA 1019
 QY 901 AAGGCTGAATTCGTTTAAAGCAAAACAGCTTGGCTTAGCAGAGGCGCAACATAACAGA 960
 DB 1020 AAGGCTGAATTCGTTTAAAGCAAAACAGCTTGGCTTAGCAGAGGCGCAACATAACAGA 1079
 QY 961 TGGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCACAGCACAGAAAAAGGTA 1020
 DB 1080 TGGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCACAGCACAGAAAAAGGTA 1139
 QY 1021 GATCTGAATGCTGATCCCTCTGTTGTAGAGAAAGAAATGGAATGAATAGCAGAAACTGCCATGC 1080

Db 1140 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGC 1199
Qy 1081 TCAGAGAACTCTAGAGATCTGAGATGTTCTCTTGGTAACACATAAATAGCAGCAATTCAG 1140
Db 1200 TCAGAGAACTCTAGAGATCTGAGATGTTCTCTTGGTAACACATAAATAGCAGCAATTCAG 1259
Qy 1141 AAAAGTTAATGAGTGGTCTTTCAGAGAGTGAATGAATGTTAGGTTCTGATGACTCACATGAT 1200
Db 1260 AAAAGTTAATGAGTGGTCTTTCAGAGAGTGAATGAATGTTAGGTTCTGATGACTCACATGAT 1319
Qy 1201 GGGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGACGTTCTAAATGAGGTAGAT 1260
Db 1320 GGGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGACGTTCTAAATGAGGTAGAT 1379
Qy 1261 GAATATTTCTGCTTCTTCAGAGAAATAGACTTACTTGGCCAGTGAATCTCATGAGGCTTTA 1320
Db 1380 GAATATTTCTGCTTCTTCAGAGAAATAGACTTACTTGGCCAGTGAATCTCATGAGGCTTTA 1439
Qy 1321 ATATGTAAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGATAATATTGAAGACAAAATA 1380
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Db 1500 TTTGGGAAAACCTATCGGAAGAGCGCAAGCCTCCCAACTTAAGCCATGAACTGAAAT 1559
Qy 1441 CTAATATAGGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1500
Db 1560 CTAATATAGGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1619
Qy 1501 AAATTAAGCGTAAAGAGAGCACTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAA 1560
Db 1620 AAATTAAGCGTAAAGAGAGCACTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAA 1679
Qy 1561 GCAGATTTGGCAGTTCAAGAGACTCTGAAATGATAATCAGGGAATCAACCAAGCGAG 1620
Db 1680 GCAGATTTGGCAGTTCAAGAGACTCTGAAATGATAATCAGGGAATCAACCAAGCGAG 1739
Qy 1621 CAGAAATGCTCAAGTGAATATTAATAATAGTGGTCAATGAGAAATAAACAAGAGTAT 1680
Db 1740 CAGAAATGCTCAAGTGAATATTAATAATAGTGGTCAATGAGAAATAAACAAGAGTAT 1799
Qy 1681 TCTATTCAGAAATGAGAAATCTTAACCCCAATGAAATCACTCGGAAAGAAATCTGCTTTC 1740
Db 1800 TCTATTCAGAAATGAGAAATCTTAACCCCAATGAAATCACTCGGAAAGAAATCTGCTTTC 1859
Qy 1741 AAAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATC 1800
Db 1860 AAAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATC 1919
Qy 1801 CACAAATTCAGAAAGCACTTAAGAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATT 1860
Db 1920 CACAAATTCAGAAAGCACTTAAGAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATT 1979
Qy 1861 CATGCGCTTGAATCTAGTAGTCACTAGAAATCTTAAGCCCACTAATTTGTAATGAAATGCAA 1920
Db 1980 CATGCGCTTGAATCTAGTAGTCACTAGAAATCTTAAGCCCACTAATTTGTAATGAAATGCAA 2039
Qy 1921 ATTGATAGTGTCTTACAGTGAAGAGATTAAGAAATAAAGTAACACCAATGCGCAGTC 1980
Db 2040 ATTGATAGTGTCTTACAGTGAAGAGATTAAGAAATAAAGTAACACCAATGCGCAGTC 2099
Qy 1981 AGGCACAGCAGAAACCTTACAACTCATCGAGAGTAAAGAACTCGCACTGAGGCGCAAGAG 2040
Db 2100 AGGCACAGCAGAAACCTTACAACTCATCGAGAGTAAAGAACTCGCACTGAGGCGCAAGAG 2159
Qy 2041 AGTAACAGCCAAATGAACAGCAAGTAAAGAGCATGACAGTATCTTTCCAGAGCTG 2100
Db 2160 AGTAACAGCCAAATGAACAGCAAGTAAAGAGCATGACAGTATCTTTCCAGAGCTG 2219
Qy 2101 AAGTTAAACAAATGCACCTGCTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAA 2160
Db 2220 AAGTTAAACAAATGCACCTGCTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAA 2279

Qy 2161 TTTGTCAATCTTAGCTTCCAGAGAGAAAGAAAGAACTAGAAAACAGTTAAAGTG 2220
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Qy 2461 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCCAGT 2520
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Qy 2581 TTTCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTTCAATCCAGGAAATGAGAGAG 2640
Db 2700 TTTCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTTCAATCCAGGAAATGAGAGAG 2759
Qy 2641 GAATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAAACAAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAAACAAAAGTCCAAAAGTCACT 2819
Qy 2701 TTTGAATGTGAACAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCCTGTA 2760
Db 2820 TTTGAATGTGAACAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCCTGTA 2879
Qy 2761 CAGACAGTTAATATCACTCAGGCTTCTGTTGTTGGTTCAGAAAGATAGCCAGTTGAT 2820
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Db 3240 TCAGCAATATTAATGAAGTAGTTCAGTATCAATATGAAAGTGGGCTCCAGTATTAATGAA 3299
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Db 5520 GGCACAGGTGTCCACCAATTGTGGTTGTGACGACAGATGCTTGGACAGAGGACAAATGGC 5579
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 Db 5580 TTCCATGCAATTGGGCGAGTGTGAGCAGCTGTGGTGCACCCGACAGAGTGGTGTGGAC 5539
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 Db 5700 AGCCACTAC 5708

RESULT 8
 AAV46466
 ID AAV46466 standard; cDNA; 5711 BP.
 XX AAV46466;
 XX 18-NOV-1998 (first entry)
 XX Human BRCA1 omi3 polymorphism #2 cDNA.
 KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 KW chromosome 17q; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 120..5711
 FT /*tag= a
 FT /product= "BRCA1 omi3 protein"
 FT 2430
 FT variation
 FT /*tag= b
 FT /note= "This polymorphic variation can be a T or C
 nucleotide"

US5750400-A.
 12-MAY-1998.
 12-FEB-1997; 97US-00798691.
 12-FEB-1996; 96US-00598591.
 (ONCO-) ONCORMED INC.
 Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
 Critz BS;
 WPI; 1998-296774/26.
 BRCA1 omi gene coding sequences - useful for distinguishing between
 polymorphisms and mutation(s) in the screening for disposition to breast
 or ovarian cancer.
 Claim 2e; Page; 54pp; English.

This sequence encodes a human BRCA1 (breast and ovarian cancer
 predisposing gene) omi3 gene in which a polymorphic variation occurs at
 nucleotide 2430. This sequence and other polymorphic variations of this
 sequence are useful for the identification of an individual who may or
 may not have an increased susceptibility to breast or ovarian cancer. The
 sequences used identify gene changes which are due to polymorphisms,
 rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 suppressor) which is involved in genetic inheritance of cancers,
 especially breast and ovarian cancer. It is found at human chromosome 17q
 which is known to be linked to cancer susceptibility, especially breast
 cancer. Cells containing a mutation in this gene lose the wild-type
 function of BRCA1 and are more susceptible to cancers. NOTE: This

CC sequence does not appear in the specification but has been created from
 CC the wild type BRCA1 omi3 gene represented in AAV46450
 XX
 SQ Sequence 5711 BP; 1953 A; 1097 C; 1277 G; 1383 T; 0 U; 1 Other;
 Query Match 100.0%; Score 5588.6; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATCGATTATTCCTCTCTTGGCGTTGAGAGAGTACAAAATGTCTAATATGCTATGCGAGAA 60
 Db 120 ATCGATTATTCCTCTCTTGGCGTTGAGAGAGTACAAAATGTCTAATATGCTATGCGAGAA 179
 Qy 61 ATCTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGGAACCTCTCTCCACAAAGTGTGAC 120
 Db 180 ATCTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGGAACCTCTCTCCACAAAGTGTGAC 239
 Qy 121 CACATATTTGCAAAATTTGTCATGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG 180
 Db 240 CACATATTTGCAAAATTTGTCATGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG 299
 Qy 181 TGTCTTTATGTAAAGATGATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGT 240
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 Qy 241 CAACTTGTTCAGAGCTATTTGAAATCAATTTGCTTTTCAGCTTCACACAGGTTGGAG 300
 Db 360 CAACTTGTTCAGAGCTATTTGAAATCAATTTGCTTTTCAGCTTCACACAGGTTGGAG 419
 Qy 301 TATGCAACAGAGCTATATTTTGCAAAAGAGGAAATAAATCTCTCTGAAACATCTAAAGAT 360
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 Db 780 GCAAAAAGAGCTGCTTGTGAAATTTCTGAGAGCGGATGTAACAAATCTGAACATCAATCAA 839
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 Db 840 CCCAGTAAATAATGATTGAAACACCACTGAGAGCGGCTGAGAGGATCCAGAAAAG 899
 Qy 781 TATCAGGGTAGTCTCTTTTCAAACTTGTGATGTGGAGCCATGTGGGCAAAATCTCATGCC 840
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 QY 5521 AGTGTAGCACTTACCAAGTGGCAGAGCTGTGACACCTACCTGTATACCCGATCCCCAC 5580
 DB 5640 AGTGTAGCACTTACCAAGTGGCAGAGCTGTGACACCTACCTGTATACCCGATCCCCAC 5699
 QY 5581 AGCCACTAC 5589
 DB 5700 AGCCACTAC 5708

RESULT 9

ID AAV46467 standard; cDNA; 5711 BP.

AC AAV46467;

XX 18-NOV-1998 (first entry)

XX Human BRCA1 omi3 polymorphism #3 cDNA.

KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 KW chromosome 17q; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 120..5711

FT /*tag= a
 FT /product= "BRCA1 omi3 protein"

FT variation 2731

FT /*tag= b

FT /note= "This polymorphic variation can be a C or T
 FT nucleotide"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-00798691.

XX 12-FEB-1996; 96US-00598591.

XX (ONCO-) ONCORMED INC.

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
 XX Critz BS;

XX WPI; 1998-296774/26.

XX BRCA1 omi gene coding sequences - useful for distinguishing between
 XX polymorphisms and mutation(s) in the screening for disposition to breast
 XX or ovarian cancer.

XX Claim 2e; Page; 54pp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer
 XX predisposing gene) omi3 gene in which a polymorphic variation occurs at
 XX nucleotide 2731. This sequence and other polymorphic variations of this
 XX sequence are useful for the identification of an individual who may or
 XX may not have an increased susceptibility to breast or ovarian cancer. The
 XX sequences used identify gene changes which are due to polymorphisms,

CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 CC suppressor) which is involved in genetic inheritance of cancers,
 CC especially breast and ovarian cancer. It is found at human chromosome 17q
 CC which is known to be linked to cancer susceptibility, especially breast
 CC cancer. Cells containing a mutation in this gene lose the wild-type
 CC function of BRCA1 and are more susceptible to cancers. NOTE: This
 CC sequence does not appear in the specification but has been created from
 CC the wild type BRCA1 omi3 gene represented in AAV46450
 XX
 XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;

Query Match 100.0%; Score 5588.6; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGATTATCTGCTCTCTCGCTTGAAGAAGTACAAAATGTCTAATATGCTATGCGAGAA 60
 DB 120 ATGGAATTAATCTGCTCTCTCGCTTGAAGAAGTACAAAATGTCTAATATGCTATGCGAGAA 179
 QY 61 ATCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 120
 DB 180 ATCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 239
 QY 121 CACATATTTGCAAAATTTTGCATGCTGAAACTTCTCAACGAGAGAAAGGGCCCTTCACAG 180
 DB 240 CACATATTTGCAAAATTTTGCATGCTGAAACTTCTCAACGAGAGAAAGGGCCCTTCACAG 299
 QY 181 TGTCTCTTTATGAAGAATGATATAACCAAAAGGAGCTTCAAGAAAGTACGAGATTAGT 240
 DB 300 TGTCTCTTTATGAAGAATGATATAACCAAAAGGAGCTTCAAGAAAGTACGAGATTAGT 359
 QY 241 CAACCTTTGAGAGCTATGAAATCTTGTGCTTTTTCAGCTTTCACACAGTTGGAG 300
 DB 360 CAACCTTTGAGAGCTATGAAATCTTGTGCTTTTTCAGCTTTCACACAGTTGGAG 419
 QY 301 TATGCAACAGAGCTATAAATTTTGCAAAAGGAGAAATAAATCTCTCTGAAACATCTAAAGAT 360
 DB 420 TATGCAACAGAGCTATAAATTTTGCAAAAGGAGAAATAAATCTCTCTGAAACATCTAAAGAT 479
 QY 361 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAT 420
 DB 480 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAT 539
 QY 421 GAACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCAAACCTCTCTAACCTTGA 480
 DB 540 GAACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCAAACCTCTCTAACCTTGA 599
 QY 481 ACTGTGAGAACTCTGAGGAAAGCAGCGGATACAAACCTCAAAAGACGCTCTGTACATT 540
 DB 600 ACTGTGAGAACTCTGAGGAAAGCAGCGGATACAAACCTCAAAAGACGCTCTGTACATT 659
 QY 541 GAATTTGGATCTGATCTCTTGAAGATACCGTTAATAGGCACTTATTCAGCTGTGGGA 600
 DB 660 GAATTTGGATCTGATCTCTTGAAGATACCGTTAATAGGCACTTATTCAGCTGTGGGA 719
 QY 601 GATCAAGAATTTGTACAAATCACCCCTCAAGGAAACGAGGATGAATCAGTTTGGATTCT 660
 DB 720 GATCAAGAATTTGTACAAATCACCCCTCAAGGAAACGAGGATGAATCAGTTTGGATTCT 779
 QY 661 GCAAAAGAGCTGCTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAA 720
 DB 780 GCAAAAGAGCTGCTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAA 839
 QY 721 CCCAGTAAATGATTTGAACACCACTGAGAGCGCTGAGAGGGGATCCAGAAAG 780
 DB 840 CCCAGTAAATGATTTGAACACCACTGAGAGCGCTGAGAGGGGATCCAGAAAG 899
 QY 781 TATCAGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATCTCATGCC 840
 DB 900 TATCAGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATCTCATGCC 959
 QY 841 AGCTCATATACAGATGAGAACAGAGCTTTATTTACTTCACTTAAAGACAGATGAATGTAGAA 900

Db 960 AGCTCATTACAGCATGAGACAGCAGTTTATTACTCACTAAGACAGAAATGAATGACAA 1019
Qy 901 AAGGCTGAATCTGTAAATAAGACAAACAGAGCTGCTTAGCAAGAGCCACATACACAGA 960
Db 1020 AAGGCTGAATCTGTAAATAAGACAAACAGAGCTGCTTAGCAAGAGCCACATACACAGA 1079
Qy 961 TGGGCTGGAAGTAAGGAACATGTAAATGATAGGCGGACTCCACGACACAGAAAAAAGGTA 1020
Db 1080 TGGGCTGGAAGTAAGGAACATGTAAATGATAGGCGGACTCCACGACACAGAAAAAAGGTA 1139
Qy 1021 GATCTGAATGCTGATCCCTGTGTCAGAGAAAGAAATGAATAGCAGAAATGCCATGC 1080
Db 1140 GATCTGAATGCTGATCCCTGTGTCAGAGAAAGAAATGAATAGCAGAAATGCCATGC 1199
Qy 1081 TCAGAGAAATCCTAGAGATACTGAAGATGTTCTTGGAATAACACTAAATAGCAGCAATTCAG 1140
Db 1200 TCAGAGAAATCCTAGAGATACTGAAGATGTTCTTGGAATAACACTAAATAGCAGCAATTCAG 1259
Qy 1141 AAGTTAATGATGCTGTTTCCAGAGTGAATGATGCTGTTAGGTTCTGATGACTCAGATGAT 1200
Db 1260 AAGTTAATGATGCTGTTTCCAGAGTGAATGATGCTGTTAGGTTCTGATGACTCAGATGAT 1319
Qy 1201 GGGGAGTCTGAATCAAAATGCCAAAGTACGATGATGATGAGGCTGTTCTAAATGAGGTAGAT 1260
Db 1320 GGGGAGTCTGAATCAAAATGCCAAAGTACGATGATGATGAGGCTGTTCTAAATGAGGTAGAT 1379
Qy 1261 GAATATCTGCTGTTCTTCAGAGAAATAGACTTACGCGCAGTGAATCCTCATGAGGCTTTA 1320
Db 1380 GAATATCTGCTGTTCTTCAGAGAAATAGACTTACGCGCAGTGAATCCTCATGAGGCTTTA 1439
Qy 1321 ATATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATA 1380
Db 1440 ATATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATA 1499
Qy 1381 TTTCGAAAACTATTCGGAAGAGCAGGCTCCCAACTTAAAGCAATGTAATCAAGAAAT 1440
Db 1500 TTTCGAAAACTATTCGGAAGAGCAGGCTCCCAACTTAAAGCAATGTAATCAAGAAAT 1559
Qy 1441 CTAATATAGCAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAT 1500
Db 1560 CTAATATAGCAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAT 1619
Qy 1501 AAATTAAGCGTAAAGAGAGCCTACATCAGGCGCTTCATCCTGAGGATTTTATCAAGAAA 1560
Db 1620 AAATTAAGCGTAAAGAGAGCCTACATCAGGCGCTTCATCCTGAGGATTTTATCAAGAAA 1679
Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAGGAACTAACCCAAACGGAG 1620
Db 1680 GCAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAGGAACTAACCCAAACGGAG 1739
Qy 1621 CAGAAATGCTCAAGTGAATGATTTACTAATAGTGGTCAATGAGATAAATAAAGAGTGAT 1680
Db 1740 CAGAAATGCTCAAGTGAATGATTTACTAATAGTGGTCAATGAGATAAATAAAGAGTGAT 1799
Qy 1681 TCTATTAGATGAGAAAAATCCCTAAACCAATAGAACTACCTGAAAAGAAATCTGCTTC 1740
Db 1800 TCTATTAGATGAGAAAAATCCCTAAACCAATAGAACTACCTGAAAAGAAATCTGCTTC 1859
Qy 1741 AAAACGAAAGTGAACCTATAAGCAGCAGATATAGCAATAGGAACTCGAAATTAATATC 1800
Db 1860 AAAACGAAAGTGAACCTATAAGCAGCAGATATAGCAATAGGAACTCGAAATTAATATC 1919
Qy 1801 CACAATTCAAAAGCACCTAAAGAAATAGGCTGAGGAGGAGTCTTCTACCGGCAATATT 1860
Db 1920 CACAATTCAAAAGCACCTAAAGAAATAGGCTGAGGAGGAGTCTTCTACCGGCAATATT 1979
Qy 1861 CATCGCTTGAATCTAGTAGTCAAGTAATCTAGGCCCACTTAATTTGATCTGAATTCGCA 1920
Db 1980 CATCGCTTGAATCTAGTAGTCAAGTAATCTAGGCCCACTTAATTTGATCTGAATTCGCA 2039
Qy 1921 ATTGATAGTTGTTCTACAGTGAAGAGATAAGAAAAAAGTACACCAATGCCAGTC 1980
Db 2040 ATTGATAGTTGTTCTACAGTGAAGAGATAAGAAAAAAGTACACCAATGCCAGTC 2099

Qy 1981 AGGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTGCAACTGAGGCCAAGAG 2040
Db 2100 AGGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTGCAACTGAGGCCAAGAG 2159
Qy 2041 AGTAAACAGCCAAATAGAAACAGACAAGTAAAGACATGACAGTGAATCTTCCCAAGAGCTG 2100
Db 2160 AGTAAACAGCCAAATAGAAACAGACAAGTAAAGACATGACAGTGAATCTTCCCAAGAGCTG 2219
Qy 2101 AAGTTTACAAATGCACCTGCTTCTTTACTAAAGTGTTCAAATCCAGTGAATCTTAAAGAA 2160
Db 2220 AAGTTTACAAATGCACCTGCTTCTTTACTTAAGTGTTCAAATCCAGTGAATCTTAAAGAA 2279
Qy 2161 TTTGTCAATCTTACCTTCCAAAGAGAGAGAAAAAGAGAGAACTAGAAAAAGTCTTAAAGT 2220
Db 2280 TTTGTCAATCTTACCTTCCAAAGAGAGAGAAAAAGAGAGAACTAGAAAAAGTCTTAAAGT 2339
Qy 2221 TCTAAATATCTCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCCAACT 2280
Db 2340 TCTAAATATCTCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCCAACT 2399
Qy 2281 GAAAGATCTCTAGAGAGTAGCAGTATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2400 GAAAGATCTCTAGAGAGTAGCAGTATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2459
Qy 2341 GAAAGTATCTCTGTTA CTGGAAGTTAGCAGTCTTAGGGAAGGCAAAAAACAGAAATATAA 2400
Db 2460 GAAAGTATCTCTGTTA CTGGAAGTTAGCAGTCTTAGGGAAGGCAAAAAACAGAAATATAA 2519
Qy 2401 TGTGTGAGTCAGTGTGCGAGCATTTGAAAAACCCCAAGGAGCTTAATTTCAATGCTGTTTCCAAA 2460
Db 2520 TGTGTGAGTCAGTGTGCGAGCATTTGAAAAACCCCAAGGAGCTTAATTTCAATGCTGTTTCCAAA 2579
Qy 2461 GATAATAGAAATGACACAGAGAGCTTTTAAATGATTCATTTGGGACATGAAAGTTAACACAGT 2520
Db 2580 GATAATAGAAATGACACAGAGAGCTTTTAAATGATTCATTTGGGACATGAAAGTTAACACAGT 2639
Qy 2521 CGGGAACAGCAGCATAGAAATGGAAGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db 2640 CGGGAACAGCAGCATAGAAATGGAAGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2699
Qy 2581 TTCAAGGTTTCAAGCGCCAGTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db 2700 TTCAAGGTTTCAAGCGCCAGTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2759
Qy 2641 GAATGTGCAACATTTCTGCGCCACTCTGCGCTCCTTAAGAGAAACAAAGTCCAAAGTCACT 2700
Db 2760 GAATGTGCAACATTTCTGCGCCACTCTGCGCTCCTTAAGAGAAACAAAGTCCAAAGTCACT 2819
Qy 2701 TTTGAATGTGAACAAAGCAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCTGTA 2760
Db 2820 TTTGAATGTGAACAAAGCAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCTGTA 2879
Qy 2761 CAGACAGTTAATATCACTGAGGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
Db 2880 CAGACAGTTAATATCACTGAGGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2939
Qy 2821 AATGCCAAATGATGATCAAGAGGCTCTAGGTTTGTGCTATCATCTCAGTTTCAGAGGC 2880
Db 2940 AATGCCAAATGATGATCAAGAGGCTCTAGGTTTGTGCTATCATCTCAGTTTCAGAGGC 2999
Qy 2881 AACGAAACTGGACTCATTTACTCCAAATAAACATGGAATTTTACAAACCCATATCCTATA 2940
Db 3000 AACGAAACTGGACTCATTTACTCCAAATAAACATGGAATTTTACAAACCCATATCCTATA 3059
Qy 2941 CCACCACTTTTCCCAATCAATTTGTTTAAATGATGAGAAATCTGCTAGAG 3000
Db 3060 CCACCACTTTTCCCAATCAATTTGTTTAAATGATGAGAAATCTGCTAGAG 3119
Qy 3001 GAAAGCTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGAATGGAATGGAATGGAATGGAAT 3060
Db 3120 GAAAGCTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGAATGGAATGGAATGGAATGGAAT 3179

QY 3061 AGTACAGTGAGCACAAATAGCGTAAATAACATTAGAGAGAAATGTTTTTAAAGAGCCAGC 3120
Db 3180 AGTACAGTGAGCACAAATAGCGTAAATAACATTAGAGAGAAATGTTTTTAAAGAGCCAGC 3239
QY 3121 TCAGCAATATTAATGAAGTGGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3180
Db 3240 TCAGCAATATTAATGAAGTGGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3299
QY 3181 ATAGGTTCCAGTGATGAAAAATCAATCAAGCAGAACTAGGTAGAAACAGAGGCGCCAAAATTG 3240
Db 3300 ATAGGTTCCAGTGATGAAAAATCAATCAAGCAGAACTAGGTAGAAACAGAGGCGCCAAAATTG 3359
QY 3241 AATGCTATGCTTAGATTAAGGGTTTGGCAACCTGAGGTCTATAACAAAGTCTTCCCTGGA 3300
Db 3360 AATGCTATGCTTAGATTAAGGGTTTGGCAACCTGAGGTCTATAACAAAGTCTTCCCTGGA 3419
QY 3301 AGTAATCTGAAGCATCTGGAATAAATAAAGCAAGAAATAGAAAGTAGTTAGACTGTT 3360
Db 3420 AGTAATCTGAAGCATCTGGAATAAATAAAGCAAGAAATAGAAAGTAGTTAGACTGTT 3479
QY 3361 AATACAGATTTCTCTCCATATCTGATTTTCAGATAACTTAGAACGCTATCGGGAAGTAGT 3420
Db 3480 AATACAGATTTCTCTCCATATCTGATTTTCAGATAACTTAGAACGCTATCGGGAAGTAGT 3539
QY 3421 CATGCATCTCAGGTTTGTCTGAGACACCTCATGACCTGTTAGATGATGGTGAATAAAG 3480
Db 3540 CATGCATCTCAGGTTTGTCTGAGACACCTCATGACCTGTTAGATGATGGTGAATAAAG 3599
QY 3481 GAAGATACGTGTTGCTGAAAAATGACATTAAGGAAGTTCTGCTGTTTTTAGCAAAAGC 3540
Db 3600 GAAGATACGTGTTGCTGAAAAATGACATTAAGGAAGTTCTGCTGTTTTTAGCAAAAGC 3659
QY 3541 GTCCAGAGGAGAGCTTAGCAGAGTCTTAGGCCCTTACCCATACACATTTGCTGCTCAG 3600
Db 3660 GTCCAGAGGAGAGCTTAGCAGAGTCTTAGGCCCTTACCCATACACATTTGCTGCTCAG 3719
QY 3601 GGTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAAGAT 3660
Db 3720 GGTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAAGAT 3779
QY 3661 GAAGGCTTCCCTGCTCCACACCTGTTATTTGTTAAAGTAAACATATACCTTCTCAG 3720
Db 3780 GAAGGCTTCCCTGCTCCACACCTGTTATTTGTTAAAGTAAACATATACCTTCTCAG 3839
QY 3721 TCTACTAGGCATAGCACGGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGAGAAATTTA 3780
Db 3840 TCTACTAGGCATAGCACGGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGAGAAATTTA 3899
QY 3781 TTATCATTTGAAGATAGCTTAATGACTGAGTAAACAGAGTAAATTTGGCAAGGATCT 3840
Db 3900 TTATCATTTGAAGATAGCTTAATGAGTAAACAGAGTAAATTTGGCAAGGATCT 3959
QY 3841 CAGGAAATACACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTTCTTACAGTGC 3900
Db 3960 CAGGAAATACACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTTCTTACAGTGC 4019
QY 3901 AGTGAATTTGGAAGCTTTGACTGCAAAATACAAACCCAGGATCCTTTCTTGAATGGTCT 3960
Db 4020 AGTGAATTTGGAAGCTTTGACTGCAAAATACAAACCCAGGATCCTTTCTTGAATGGTCT 4079
QY 3961 TCCAAACAAATGAGGCAATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGCAGAGAAATTG 4020
Db 4080 TCCAAACAAATGAGGCAATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGCAGAGAAATTG 4139
QY 4021 GTTTTCAGATGATGAAGAAAGAGGAAACCGGCTTGAAGAAATATCAAGAGAGCAAGC 4080
Db 4140 GTTTTCAGATGATGAAGAAAGAGGAAACCGGCTTGAAGAAATATCAAGAGAGCAAGC 4199
QY 4081 ATGGATTCAAACTTAGGTGAAGAGAGCATCTGGGTGAGAGTGAACCAAGGCTCTGAA 4140
Db 4200 ATGGATTCAAACTTAGGTGAAGAGAGCATCTGGGTGAGAGTGAACCAAGGCTCTGAA 4259
QY 4141 GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATG 4200

Db 4260 GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATG 4319
QY 4201 CACATTAACCTGATTAAGCTCCAGCAGGAAATGGCTGAACTGAAGCTGTGTAGAACAG 4260
Db 4320 CACATTAACCTGATTAAGCTCCAGCAGGAAATGGCTGAACTGAAGCTGTGTAGAACAG 4379
QY 4261 CATGGGAGCCAGCCTTTCTAAACAGCTACCTTCCATCATAAAGTCACTCTTCTGCCCTTGAG 4320
Db 4380 CATGGGAGCCAGCCTTTCTAAACAGCTACCTTCCATCATAAAGTCACTCTTCTGCCCTTGAG 4439
QY 4321 GACTGCGAATCCAGAACAAAGACATCAGAAAGACAGTATTAACCTTCCAGAAAGT 4380
Db 4440 GACTGCGAATCCAGAACAAAGACATCAGAAAGACAGTATTAACCTTCCAGAAAGT 4499
QY 4381 AGTGAATACCTCTAAGCCAGAAATCCAGAGGCTTTCTGCTCAGCAAGTTTGAAGTGTCT 4440
Db 4500 AGTGAATACCTCTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTGAAGTGTCT 4559
QY 4441 GCAGATAGTTCTTACAGTAAAGAAACAGAGAGTGGAAAGGTCTATCCCTTCTAAA 4500
Db 4560 GCAGATAGTTCTTACAGTAAAGAAACAGAGAGTGGAAAGGTCTATCCCTTCTAAA 4619
QY 4501 TGCCCATCATTTAGATGATAGTGTGCTACATGACAGTTGCTCTGGAGTCTTCAAGATAGA 4560
Db 4620 TGCCCATCATTTAGATGATAGTGTGCTACATGACAGTTGCTCTGGAGTCTTCAAGATAGA 4679
QY 4561 AACTACCCATCTCAAGAGGAGCTCAATTAAGTTGTTGATGTGGAGAGCAACAGCTGGAA 4620
Db 4680 AACTACCCATCTCAAGAGGAGCTCAATTAAGTTGTTGATGTGGAGAGCAACAGCTGGAA 4739
QY 4621 GAGTCTGGGCGCACACCATTTGACGGAACATCTTACTTCCCAAGGCAAGATCTAGAGGA 4680
Db 4740 GAGTCTGGGCGCACACCATTTGACGGAACATCTTACTTCCCAAGGCAAGATCTAGAGGA 4799
QY 4681 ACCCTTACCTGGAATCTGGAATFAGCTCTTCTCTGATGACCTTGAATCTGATCTCTTCT 4740
Db 4800 ACCCTTACCTGGAATCTGGAATFAGCTCTTCTCTGATGACCTTGAATCTGATCTCTTCT 4859
QY 4741 GAAGACAGAGCCCCAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTTGCATTG 4800
Db 4860 GAAGACAGAGCCCCAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTTGCATTG 4919
QY 4801 AAAGTTCCCAATTTGAAAGTTGAGAAATCTGCCAGGGTCCAGCTGCTGCTCATATCTACT 4860
Db 4920 AAAGTTCCCAATTTGAAAGTTGAGAAATCTGCCAGGGTCCAGCTGCTGCTCATATCTACT 4979
QY 4861 GATCTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGAGAGCCAGAAATGACA 4920
Db 4980 GATCTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGAGAGCCAGAAATGACA 5039
QY 4921 GCTTCAACAGAAAGGTTCAACAAAGAAATGCTCCATGCTGTGTGCTGGCTGACCCAGAA 4980
Db 5040 GCTTCAACAGAAAGGTTCAACAAAGAAATGCTCCATGCTGTGTGCTGGCTGACCCAGAA 5099
QY 4981 GAATTTATGCTGCTGTAACAAGTTTGCAGAAACACCAATCACTTTAACTTAATCTAAAT 5040
Db 5100 GAATTTATGCTGCTGTAACAAGTTTGCAGAAACACCAATCACTTTAACTTAATCTAAAT 5159
QY 5041 ACTGAAAGAGTACTCATGTTGTTAAGAAACAGATGCTGAGTTGTTGTTGTAACCGACA 5100
Db 5160 ACTGAAAGAGTACTCATGTTGTTAAGAAACAGATGCTGAGTTGTTGTTGTAACCGACA 5219
QY 5101 CTGAAATATTTTCTAGGAAATTCGGGAGGAAATTCGGTGTAGTCTTATTTCTGGGTGACC 5160
Db 5220 CTGAAATATTTTCTAGGAAATTCGGGAGGAAATTCGGTGTAGTCTTATTTCTGGGTGACC 5279
QY 5161 CAGTCTTATTAAGAAAGAAATGCTGATGAGCATGATTTTCAAGTCAAGAGAGATG 5220
Db 5280 CAGTCTTATTAAGAAAGAAATGCTGATGAGCATGATTTTCAAGTCAAGAGAGATG 5339
QY 5221 GTCAATGGAGAGAAACCAACAGGTCCTCAAGCAGAGCAAGAGATCCAGAGACAGAAAGATC 5280

5340 GTCAATGGAGAAACCCACCAAGGTCCAAAGCGAGCAAGAGATCCACGACAGAAAGATC 5399
5281 TTCAGGGGCTAGAAATCTGTGCTATGGGCGCTTCAACCAATGCCACAGATCAATCG 5340
5400 TTCAGGGGCTAGAAATCTGTGCTATGGGCGCTTCAACCAATGCCACAGATCAATCG 5459
5341 GAATGGATGGTACAGCTGTGTGGTCTTCTGTGGTGAAGAGCTTTTCATCTTACCCCTT 5400
5460 GAATGGATGGTACAGCTGTGTGGTCTTCTGTGGTGAAGAGCTTTTCATCTTACCCCTT 5519
5401 GGCACAGGTGTCACCCAAATTTGGTGTGGTGGAGCCAGATGCTTGGACAGAGACAATGGC 5460
5520 GGCACAGGTGTCACCCAAATTTGGTGTGGTGGAGCCAGATGCTTGGACAGAGACAATGGC 5579
5461 TTCCATGCAATTTGGGCGAGATGTGAGGCACTGTGTGGTGGAGAGCTTTTCATCTTACCCCTT 5520
5580 TTCCATGCAATTTGGGCGAGATGTGAGGCACTGTGTGGTGGAGAGCTTTTCATCTTACCCCTT 5639
5521 AGTGTAGCACTTACCAAGTGCAGGAGCTGGACACTTACCTGATACCCCGAGATCCCCCAC 5580
5640 AGTGTAGCACTTACCAAGTGCAGGAGCTGGACACTTACCTGATACCCCGAGATCCCCCAC 5699
5581 AGCCACTAC 5589
5700 AGCCACTAC 5708

RESULT 10
AAV46469
ID AAV46469 standard; cDNA; 5711 BP.
AC AAV46469;
XX
DT 18-NOV-1998 (first entry)
XX Human BRCA1 omi3 polymorphism #5 cDNA.
XX
KW BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT /*tag= a
FT /product= "BRCA1 omi3 protein"
FT variation 3667
FT /*tag= b
FT /note= "This polymorphic variation can be an A or G
nucleotide"

US5750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-00798691.
XX
XX 12-FEB-1996; 96US-00598591.
XX (ONCO-) ONCORMED INC.
XX
XX Olson SJ, Murphy PJ, Zeng B, Alvares CP, Scheiter DB, Allen AC;
XX Critz BS;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.
XX
XX Claim 2e; Page; 54pp; English.

This sequence encodes a human BRCA1 (breast and ovarian cancer predisposing gene) omi3 gene in which a polymorphic variation occurs at nucleotide 3667. This sequence and other polymorphic variations of this sequence are useful for the identification of an individual who may or may not have an increased susceptibility to breast or ovarian cancer. The sequences used identify gene changes which are due to polymorphisms, rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour suppressor) which is involved in genetic inheritance of cancers, especially breast and ovarian cancer. It is found at human chromosome 17q which is known to be linked to cancer susceptibility, especially breast cancer. Cells containing a mutation in this gene lose the wild-type function of BRCA1 and are more susceptible to cancers. NOTE: This sequence does not appear in the specification but has been created from the wild type BRCA1 omi3 gene represented in AAV46450

XX Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;
SQ

Query Match 100.0%; Score 5588.6; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTTATCTGCTCTTCGCTTGAAGAGTACAAAATGTCATTATGCTATGCAGAAA 60
Db |||||
Qy 120 ATGGATTTATCTGCTCTTCGCTTGAAGAGTACAAAATGTCATTATGCTATGCAGAAA 179
Db |||||
Qy 61 ATCTTAGAGTCTCCCATCTGTCTGGAGTTCATCAAGCAAGCTGTCTCCCAAAAGTGTGAC 120
Db |||||
Qy 180 ATCTTAGAGTCTCCCATCTGTCTGGAGTTCATCAAGCAAGCTGTCTCCCAAAAGTGTGAC 239
Db |||||
Qy 121 CACATATTTTGCATAATTTTCATGCTGAAACTTCTCAACAGAGAAAGGCGCTTTCACAG 180
Db |||||
Qy 240 CACATATTTTGCATAATTTTCATGCTGAAACTTCTCAACAGAGAAAGGCGCTTTCACAG 299
Db |||||
Qy 181 TGTCTTTATGTAGATATATATAACCAAGAGAGCTTCAAGAAAGTACAGATTTAGT 240
Db |||||
Qy 300 TGTCTTTATGTAGATATATATAACCAAGAGAGCTTCAAGAAAGTACAGATTTAGT 359
Db |||||
Qy 241 CAATCTTTCAGAGCTATTTGAAAATCATTTTGTCTTTTTCAGTTGACAGGTTTTCAG 300
Db |||||
Qy 360 CAATCTTTCAGAGCTATTTGAAAATCATTTTGTCTTTTTCAGTTGACAGGTTTTCAG 419
Db |||||
Qy 301 TATGCAAAAGCTATATATTTTGCAAAAGAGAAATAAATCTCTCTGAACATCTTAAAGAT 360
Db |||||
Qy 420 TATGCAAAAGCTATATATTTTGCAAAAGAGAAATAAATCTCTCTGAACATCTTAAAGAT 479
Db |||||
Qy 361 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGATTTTACAGAGT 420
Db |||||
Qy 480 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGATTTTACAGAGT 539
Db |||||
Qy 421 GAACCCGAAAATCCTTCTCTGAGGAAAACAGTCTCAGTGTCCAACTCTTACCTTGA 480
Db |||||
Qy 540 GAACCCGAAAATCCTTCTCTGAGGAAAACAGTCTCAGTGTCCAACTCTTACCTTGA 599
Db |||||
Qy 481 ACTGTGAGAACTCTGAGGACAAAGCGGATACAACTTCAAAAGAGCTGTCTTACATT 540
Db |||||
Qy 600 ACTGTGAGAACTCTGAGGACAAAGCGGATACAACTTCAAAAGAGCTGTCTTACATT 659
Db |||||
Qy 541 GAATTTGGATCTGATTTCTTCTGAAGTACCGTTAATAAGCAACTTATTCAGTGTGGGA 600
Db |||||
Qy 660 GAATTTGGATCTGATTTCTTCTGAAGTACCGTTAATAAGCAACTTATTCAGTGTGGGA 719
Db |||||
Qy 601 GATCAAGAAATTTGTTACAAATTCACCTCAAGGAAACAGGATCAAAATCAGTTTGAATTCT 660
Db |||||
Qy 720 GATCAAGAAATTTGTTACAAATTCACCTCAAGGAAACAGGATCAAAATCAGTTTGAATTCT 779
Db |||||
Qy 661 GCAAAAAGGCTGCTGTGATTTTCTGAGAAGGATGTAAACAAATCTGAACATCATCAA 720
Db |||||
Qy 780 GCAAAAAGGCTGCTGTGATTTTCTGAGAAGGATGTAAACAAATCTGAACATCATCAA 839
Db |||||
Qy 721 CCGAGTAAATGATTTGATTAACCACTGAGAGAGCGTGCAGCTGAGAGGATCCAGAAAAG 780
Db |||||
Qy 840 CCGAGTAAATGATTTGATTAACCACTGAGAGAGCGTGCAGCTGAGAGGATCCAGAAAAG 899
Db |||||

QY 781 TATCAGGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCC 840
Db 900 TATCAGGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCC 959
QY 841 AGCTCAATACAGCATGAGCAACAGCAGTTTATTACTCACTTAAGACAGAAATCAATGTAGAA 900
Db 960 AGCTCAATACAGCATGAGCAACAGCAGTTTATTACTCACTTAAGACAGAAATCAATGTAGAA 1019
QY 901 AAGGCTGAATCTGTATAAAGCAAAACAGCCTGGCTTAGCAGAGCCAACTAAACAGA 960
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QY 961 TGGGCTGGAAGTAAAGCAAACTGTAAATGATAGGCGGACTCCAGACACAGAAAAAAGGTA 1020
Db 1080 TGGGCTGGAAGTAAAGCAAACTGTAAATGATAGGCGGACTCCAGACACAGAAAAAAGGTA 1139
QY 1021 GATCTGAATGCTGATGCCCTGTGTGAGAGAAAAAAGTAATGGAATAGCAAACTGCCATGC 1080
Db 1140 GATCTGAATGCTGATGCCCTGTGTGAGAGAAAAAAGTAATGGAATAGCAAACTGCCATGC 1199
QY 1081 TCAGAGAACTCTAGAGATCTGAACATGTTCTCTGGATAACACATAATAGCAGCATTCAG 1140
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Db 1380 GAAATATCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCTCTCATGAGCGCTTTA 1439
QY 1321 ATATGTAAGAGTGAAGAGTTTCACTCCAAATCAGTAGAGATATATTTGAAGACAAATA 1380
Db 1440 ATATGTAAGAGTGAAGAGTTTCACTCCAAATCAGTAGAGATATATTTGAAGACAAATA 1499
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Db 1500 TTGGGAAAACTATCGGAGAGGCAAGCTCCGCCAATTTAAGCCATGTAACATGNAAT 1559
QY 1441 CTAATATAGAGGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1500
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QY 1801 CACAATTCAAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTACGAGCATATT 1860
Db 1920 CACAATTCAAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTACGAGCATATT 1979
QY 1861 CATGGCTTGAACCTAGTAGTCAAGTAGAATCTAAGGCCCACTAATTTGATGTGAATTGCAA 1920

Db 1980 CATGGCTTGAACCTAGTAGTCAAGTAGAATCTAAGGCCCACTAATTTGTACTGAATTGCAA 2039
QY 1921 ATTGATAGTTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTC 1980
Db 2040 ATTGATAGTTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTC 2099
QY 1981 AGGCACAGCAAAACCTTAGCAACTCTGGAAGGTAAAGAACTTCAACTGAGGCAAGAG 2040
Db 2100 AGGCACAGCAAAACCTTAGCAACTCTGGAAGGTAAAGAACTTCAACTGAGGCAAGAG 2159
QY 2041 AGTAACAAGCCAAATGAACAGACAGAGTAAAGACATGACAGAGTGATATCTTCCAGAGCTG 2100
Db 2160 AGTAACAAGCCAAATGAACAGACAGAGTAAAGACATGACAGAGTGATATCTTCCAGAGCTG 2219
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QY 2461 GATAATAGAAATCACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCACT 2520
Db 2580 GATAATAGAAATCACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCACT 2639
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QY 2641 GAATGTCACATTTCTTCCGCCACTCTGGTCTTTAAGAAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTCACATTTCTTCCGCCACTCTGGTCTTTAAGAAACAAAGTCCAAAAGTCACT 2819
QY 2701 TTTGAAATGTAACAAAGGAGAAATCAAGGAAAGAGTGAATGAGTCTTAATATCAAGCCTGA 2760
Db 2820 TTTGAAATGTAACAAAGGAGAAATCAAGGAAAGAGTGAATGAGTCTTAATATCAAGCCTGA 2879
QY 2761 CAGACAGTTAAATCACTCAGGCGTTCTCTGTTGTTGGTTCAGAAAGATAGCCAGTTGAT 2820
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QY 2821 AATGCCAAATGATATCAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGC 2880
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Db 3000 AACGAACCTGGACTCAATTAATCAATAAATGAGCTTTTTCAGAAACCAATATCTGATA 3059
QY 2941 CCACCACTTTTCCCAATCAAGTCAATTTGTTTAAAACTAAATGTAAGAAAAATCTGCTAGAG 3000

Db 3060 CCACCACCTTTTCCCATCAAGTCATTTGTTAAATCTAAATCTAAGAAAAATCTCTAGAG 3119
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Db 3120 GAAAACTTTGAGGAACATTTCAATGTCACTCAAGAGAGAAATGGGAATGAGAACATTTCCA 3179
Qy 3061 AGTACAGTACGACAAATTTAGCGGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGC 3120
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Qy 3121 TCAAGCAATATTAATGAATAGTGGTTCCAGTACTAATGAATGGGCTCCAGTAAATTAAGAA 3180
Db 3240 TCAAGCAATATTAATGAATAGTGGTTCCAGTACTAATGAATGGGCTCCAGTAAATTAAGAA 3299
Qy 3181 ATAGGTTCCAGTATGAAAAATTTCAAGCAGAACTTAGTGAAGAACAGAGGCCCCAAAATTG 3240
Db 3300 ATAGGTTCCAGTATGAAAAATTTCAAGCAGAACTTAGTGAAGAACAGAGGCCCCAAAATTG 3359
Qy 3241 AATGCTATGTTAGATTAAGGTTTTCGAACCTGAGGCTCTATAACAAAGTCTTCCCTGGA 3300
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Qy 3301 AGTAATTTGTAAGCATCTCTGAAATATAAAGCAAGATATGAAGAGTAGTTTCAGACTGTT 3360
Db 3420 AGTAATTTGTAAGCATCTCTGAAATATAAAGCAAGATATGAAGAGTAGTTTCAGACTGTT 3479
Qy 3361 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCCTATGGGAAGTAGT 3420
Db 3480 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCCTATGGGAAGTAGT 3539
Qy 3421 CATGCACTCTAGGTTTGTCTGAGACACCTGATGACCTGTTTAGATGATGTTGAATTAAG 3480
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Qy 3481 GAAGATCTAGTTTGTGCAAAATGACATTAAGGAAGTTCTGCTGTTTTTAGCAAAAGC 3540
Db 3600 GAAGATCTAGTTTGTGCAAAATGACATTAAGGAAGTTCTGCTGTTTTTAGCAAAAGC 3659
Qy 3541 GTCCAGAGAGGAGAGCTTAGCAGAGTCTTAGCCCTTCAACCATAACATTTGGCTCAG 3600
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Qy 3601 GGTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGAT 3660
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Db 3780 GAAGAGCTTCCTGCTTCCAACTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG 3839
Qy 3721 TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTA 3780
Db 3840 TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTA 3899
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Qy 4081 ATGGAATTCRAACTTAGTGAAGCAGCATCTCTGGGTGTGAGAGTGAACAACAGCGTCTCTGAA 4140
Db 4200 ATGGAATTCRAACTTAGTGAAGCAGCATCTCTGGGTGTGAGAGTGAACAACAGCGTCTCTGAA 4259
Qy 4141 GACTGTCTCAGGGCTATCTCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG 4200
Db 4260 GACTGTCTCAGGGCTATCTCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG 4319
Qy 4201 CAACATAACCTGATATAAGCTCCAGAGGAAATGGCTGAACTAGAACTGTGTTAGAACAG 4260
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Qy 4261 CATGGAGGAGCAGCTTTTAAACAGCTACCTTCCATCATTAAGTCACTCTTCTGCCCTTGAG 4320
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Qy 5041 ACTGAGAGACTACTCATCTGTTATGAAAACAGATGCTGAGTGTGTTGTGAAACGACAA 5100
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Qy 5101 CTGAAATATTTTCTAGGAATTCGGGAGGAAATGGTATGTTAGCTATTTCTGGGTGACC 5160
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Db 1980 CATGCGCTTTGAACTAGTACTAGTACAAATCTTAAGCCCACTTAATTTGTACTGAAATGCAA 2039
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Db 2880 CAGACAGTATATATCAGTGGAGGCTTTCTCTGTTGGTGGTTCAGAAAGATAAGCCAGTTGAT 2939
Qy 2821 AATGCCAAATGTAGTATCAAGAGGAGGCTCTAGGTTTTGCTCTATCATCTCAGTTTCAGAGGC 2880
Db 2940 AATGCCAAATGTAGTATCAAGAGGAGGCTCTAGGTTTTGCTCTATCATCTCAGTTTCAGAGGC 2999

Db 5160 ACTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTAACGGACA 5219
Qy 5101 CTGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTCTCGGTGACC 5160
Db 5220 CTGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTCTCGGTGACC 5279
Qy 5161 CAGTCTATTAAAGAAAGAAATGCTGAATCAGCATGATTTTGAAGTCAGAGGAGATGTG 5220
Db 5280 CAGTCTATTAAAGAAAGAAATGCTGAATCAGCATGATTTTGAAGTCAGAGGAGATGTG 5339
Qy 5221 GTCATATGAAGAAACCAAGAGTCCAAAGCGAGAAAGAGATCCCGAGGACAGAAAGATC 5280
Db 5340 GTCATATGAAGAAACCAAGAGTCCAAAGCGAGAAAGAGATCCCGAGGACAGAAAGATC 5399
Qy 5281 TTCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCCACACATGCCACAGATCAACTG 5340
Db 5400 TTCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCCACACATGCCACAGATCAACTG 5459
Qy 5341 GAATGATGTGTACAGCTGTGTGCTCTGTGTGAGGAGCTTTTCATCATCCACCTT 5400
Db 5460 GAATGATGTGTACAGCTGTGTGCTCTGTGTGAGGAGCTTTTCATCATCCACCTT 5519
Qy 5401 GGCACAGGTGTCACCCCAATTTGCTGTGCGAGCAGATGCTGTGAGGAGGAGGAGGAGG 5460
Db 5520 GGCACAGGTGTCACCCCAATTTGCTGTGCGAGCAGATGCTGTGAGGAGGAGGAGGAGG 5579
Qy 5461 TTCATGCAATTTGGGCGAGATGTGTAGGCGACCTGTGTGTGACCCGAGAGTGGGTGGAC 5520
Db 5580 TTCATGCAATTTGGGCGAGATGTGTAGGCGACCTGTGTGTGACCCGAGAGTGGGTGGAC 5639
Qy 5521 AGTGTAGACTCTACAGAGTCCAGAGTGTGACACTTACCTGATACCCAGATCCCCAC 5580
Db 5640 AGTGTAGACTCTACAGAGTCCAGAGTGTGACACTTACCTGATACCCAGATCCCCAC 5699
Qy 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 12
ID AAV46471 standard; cDNA; 5711 BP.
XX AC AAV46471;
XX
XX 18-NOV-1998 (first entry)
XX Human BRCA1 omi3 polymorphism #7 cDNA.
XX
XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 120..5711
XX /*tag= a
XX /product= "BRCA1 omi3 protein"
XX variation 4956
XX /*tag= b
XX /note= "This polymorphic variation can be an A or G
XX nucleotide"
XX
XX US5750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-00798691.
XX
XX 12-FEB-1996; 96US-00598591.
XX
XX (ONCO-) ONCORMED INC.

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
PI Critz BS;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.
XX
XX Claim 2e; Page; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi3 gene in which a polymorphic variation occurs at
XX nucleotide 4956. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer. The
XX sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome 17q
XX which is known to be linked to cancer susceptibility, especially breast
XX cancer. Cells containing a mutation in this gene lose the wild-type
XX function of BRCA1 and are more susceptible to cancers. NOTE: This
XX sequence does not appear in the specification but has been created from
XX the wild type BRCA1 omi3 gene represented in AAV46450
XX
SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;
Query Match 100.0%; Score 5588.6; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGATTTATCTGCTCTTCGCGTTGAAGAAAGTACAAAATGTCTAATATGCTATGCAGAAA 60
Db 120 ATGATTTATCTGCTCTTCGCGTTGAAGAAAGTACAAAATGTCTAATATGCTATGCAGAAA 179
Qy 61 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGAC 120
Db 180 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGAC 239
Qy 121 CACATATTTGCAAAATTTTGGCATGCTGAACTTTCTCAACGAGAAAGGGCTTCACAG 180
Db 240 CACATATTTGCAAAATTTTGGCATGCTGAACTTTCTCAACGAGAAAGGGCTTCACAG 299
Qy 181 TGTCTTTATGTAAGATGATATATAACCAAAAGAGGCTTACAAAGAAAGTACGAGATTAGT 240
Db 300 TGTCTTTATGTAAGATGATATATAACCAAAAGAGGCTTACAAAGAAAGTACGAGATTAGT 359
Qy 241 CAACTTTTGAAGAGCTATTGAATTCATTTCTGCTTTTTCAGCTTGACACAGGTTGGAG 300
Db 360 CAACTTTTGAAGAGCTATTGAATTCATTTCTGCTTTTTCAGCTTGACACAGGTTGGAG 419
Qy 301 TATGCAAAACAGCTATAAATTTTGCAAAAAGGAAATAACTCTCTCGAATCTTAAAGAT 360
Db 420 TATGCAAAACAGCTATAAATTTTGCAAAAAGGAAATAACTCTCTCGAATCTTAAAGAT 479
Qy 361 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAT 420
Db 480 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAT 539
Qy 421 GAACCCGAAAAATCTCTTCTGAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGA 480
Db 540 GAACCCGAAAAATCTCTTCTGAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGA 599
Qy 481 ACTGTGAGAACTCTGAGGAAACAGGAGGAGATACAACTCAAAAGAGCTCTGTCTACATT 540
Db 600 ACTGTGAGAACTCTGAGGAAACAGGAGGAGATACAACTCAAAAGAGCTCTGTCTACATT 659
Qy 541 GAATTGGGATCTGATTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCGAGTGGGA 600
Db 660 GAATTGGGATCTGATTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCGAGTGGGA 719

QY 601 GATCAGAAATGTTTACAAATCACCCTCAGAGAACCGAGGATGAATCAGTTGGATTCT 660
DB 720 GATCAGAAATGTTTACAAATCACCCTCAGAGAACCGAGGATGAATCAGTTGGATTCT 779
QY 661 GCAAAAAGGCTGCTTGTGAATTTCTGACAGCGATGTAACAAATAGTGAACATCATCAA 720
DB 780 GCAAAAAGGCTGCTTGTGAATTTCTGACAGCGATGTAACAAATAGTGAACATCATCAA 839
QY 721 CCCAGTAATTAATGATGAACACCACTGAGAGAGCGTGCAGCTGAGAGCGATCCGANAAG 780
DB 840 CCCAGTAATTAATGATGAACACCACTGAGAGAGCGTGCAGCTGAGAGCGATCCGANAAG 899
QY 781 TATCAGGCTAGTCTCTGTTTCAAACTTGCACTGAGAGCGATGTCACAAATACTCATGCC 840
DB 900 TATCAGGCTAGTCTCTGTTTCAAACTTGCACTGAGAGCGATGTCACAAATACTCATGCC 959
QY 841 AGCTCATTAAGCATGAGAGAGCAGCAGTTTATTAATCTCACTAAGACAGAAATGTAAGAA 900
DB 960 AGCTCATTAAGCATGAGAGAGCAGCAGTTTATTAATCTCACTAAGACAGAAATGTAAGAA 1019
QY 901 AAGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTAGCAAGGAGCCCAACATAACAGA 960
DB 1020 AAGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTAGCAAGGAGCCCAACATAACAGA 1079
QY 961 TGGCTCGAAGTAAGGAAAACATGTAATGATAGGCGGACTCCAGCAAGAAAAAGGTA 1020
DB 1080 TGGCTCGAAGTAAGGAAAACATGTAATGATAGGCGGACTCCAGCAAGAAAAAGGTA 1139
QY 1021 GATCTGAATGCTGATCCCTGCTGTGAGAGAGAAAGATGGAATAGCAGAACTGCCATGC 1080
DB 1140 GATCTGAATGCTGATCCCTGCTGTGAGAGAGAAAGATGGAATAGCAGAACTGCCATGC 1199
QY 1081 TCAGAGAACTCCTAGAGATGTAAGATGTTCTTTGGATACACTAATAAGCAGCATTCAG 1140
DB 1200 TCAGAGAACTCCTAGAGATGTAAGATGTTCTTTGGATACACTAATAAGCAGCATTCAG 1259
QY 1141 AAGGTAATGCTGTTTCCAGAGAGTGAATGAACTGTTAGGTTCTGATGATCTCAGATGAT 1200
DB 1260 AAGGTAATGCTGTTTCCAGAGAGTGAATGAACTGTTAGGTTCTGATGATCTCAGATGAT 1319
QY 1201 GGGGAGTCTGAATCAAAATGCCAAATAGTCTGATGATATTTGAGCGTTCTTAATGAGGTAGAT 1260
DB 1320 GGGGAGTCTGAATCAAAATGCCAAATAGTCTGATGATATTTGAGCGTTCTTAATGAGGTAGAT 1379
QY 1261 GAATATTTCTGTTCTTCAGAGAAATAGACTTACTGCGAGTATCTCATGAGGCTTTA 1320
DB 1380 GAATATTTCTGTTCTTCAGAGAAATAGACTTACTGCGAGTATCTCATGAGGCTTTA 1439
QY 1321 ATATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGATATATTTGAAGCAAAATA 1380
DB 1440 ATATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGTATATTTGAAGCAAAATA 1499
QY 1381 TTTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCCATGTAACCTGAATAAT 1440
DB 1500 TTTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCCATGTAACCTGAATAAT 1559
QY 1441 CTAATTAAGAGCAATTTGTTACTGAGCAGCAGATATACAGAGCGTCCCTCCACAAAT 1500
DB 1560 CTAATTAAGAGCAATTTGTTACTGAGCAGCAGATATACAGAGCGTCCCTCCACAAAT 1619
QY 1501 AAATTAAGCGTAAAGAGAGCCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAA 1560
DB 1620 AAATTAAGCGTAAAGAGAGCCTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAA 1679
QY 1561 GCAGATTCGAGTTCAAAAGACTCCCTGAATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1680 GCAGATTCGAGTTCAAAAGACTCCCTGAATGATGATGATGATGATGATGATGATGATGAT 1739
QY 1621 CAGAAATGCTCAAGTGAATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1740 CAGAAATGCTCAAGTGAATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1799
QY 1681 TCTATTAGATGAGAAAAATCCTTAACCCCAATAGATCACTCGAAAAAGAAATCTGCTTTC 1740

DB 1800 TCTATTAGATGAGAAAAATCCTTAACCCCAATAGATCACTCGAAAAAGAAATCTGCTTTC 1859
QY 1741 AAAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATCGAACTCGAATTAATATC 1800
DB 1860 AAAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATCGAACTCGAATTAATATC 1919
QY 1801 CCAATTTCAAAAGCAGCCTTAAGAAATAGGCTGAGAGGAGCTCTCTACAGGCAATTT 1860
DB 1920 CCAATTTCAAAAGCAGCCTTAAGAAATAGGCTGAGAGGAGCTCTCTACAGGCAATTT 1979
QY 1861 CATGCCCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTTGTAATGTAATGCAA 1920
DB 1980 CATGCCCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTTGTAATGTAATGCAA 2039
QY 1921 ATTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACAAACCAATGCCAGTC 1980
DB 2040 ATTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACAAACCAATGCCAGTC 2099
QY 1981 AGGCACAGCAGAAACCTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGCCAGAAAG 2040
DB 2100 AGGCACAGCAGAAACCTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGCCAGAAAG 2159
QY 2041 AGTAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGATATCTTTCCAGAGCTG 2100
DB 2160 AGTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGATATCTTTCCAGAGCTG 2219
QY 2101 AGTTTAAACAAATGACCTGTTCTTTTACTAGTGTCAAAATACCACTGTAATTAAGAA 2160
DB 2220 AGTTTAAACAAATGACCTGTTCTTTTACTAGTGTCAAAATACCACTGTAATTAAGAA 2279
QY 2161 TTTGTCATCTTCAAGCTTCCAAAGAGAAAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2220
DB 2280 TTTGTCATCTTCAAGCTTCCAAAGAGAAAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2339
QY 2221 TCTTAATAATGCTGAGAGCCCAAGATCTCATGTTTAAAGTGAAGAGGTTTTCGAACT 2280
DB 2340 TCTTAATAATGCTGAGAGCCCAAGATCTCATGTTTAAAGTGAAGAGGTTTTCGAACT 2399
QY 2281 GAAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2340
DB 2400 GAAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2459
QY 2341 GAAAGTATCTGTTACTGGAAGTACCTCTAGGAGAGGCAAAACAGAAACCAATATA 2400
DB 2460 GAAAGTATCTGTTACTGGAAGTACCTCTAGGAGAGGCAAAACAGAAACCAATATA 2519
QY 2401 TGTGTGAGTCAAGTGTGAGCATTTGAAAAACCCCAAGGGACTAATTCATGTTGTTCCAAA 2460
DB 2520 TGTGTGAGTCAAGTGTGAGCATTTGAAAAACCCCAAGGGACTAATTCATGTTGTTCCAAA 2579
QY 2461 GATAATAGAAATGACACAGAGCGTTTAAAGTATCCATTGGGACATGAGTTAACACAGT 2520
DB 2580 GATAATAGAAATGACACAGAGCGTTTAAAGTATCCATTGGGACATGAGTTAACACAGT 2639
QY 2521 CGGGAACCAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGAGAGATACA 2580
DB 2640 CGGGAACCAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGAGAGATACA 2699
QY 2581 TTCAGGTTTCAAGCGCCAGTCATTTGCTCTGTTTTTCAATCCAGGAAATGAGAGAG 2640
DB 2700 TTCAGGTTTCAAGCGCCAGTCATTTGCTCTGTTTTTCAATCCAGGAAATGAGAGAG 2759
QY 2641 GAATGTCAACATCTCTGCCACTCTGGGTCTTAAAGAAACCAAGTCCAAAAGTCACT 2700
DB 2760 GAATGTCAACATCTCTGCCACTCTGGGTCTTAAAGAAACCAAGTCCAAAAGTCACT 2819
QY 2701 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCTGTA 2760
DB 2820 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCTGTA 2879
QY 2761 CAGACAGTTTAAATATCACTGAGGCTTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2820

Db	2880	CAGACAGTTAATATACATCGCAGGCTTTCTCCTGTGGTTGGTCTAGAAAGATATAGCCAGTTGAT	2939
Qy	2821	AATGCCAAATCTAGTATATCAAAAGGAGGCTCTAGGTTTGTCTTATCATCTCAGTTCAGAGGC	2880
Db	2940	AATGCCAAATCTAGTATCAAAAGGAGGCTCTAGGTTTGTCTTATCATCTCAGTTCAGAGGC	2999
Qy	2881	AACGAAATCGACTTCATTACTCCGAATAAACAATGGACTTTTACAAAACCCATATCGTATA	2940
Db	3000	AACGAAATCGACTTCATTACTCCGAATAAACAATGGACTTTTACAAAACCCATATCGTATA	3059
Qy	2941	CCAGCATTTTTCCCATCAAGTCAATTTCTTTAAACTAAATGTAAAGAAAAATCTCTAGAG	3000
Db	3060	CCAGCATTTTTCCCATCAAGTCAATTTCTTTAAACTAAATGTAAAGAAAAATCTCTAGAG	3119
Qy	3001	GA AAAA CTTTGAGGAACATTTCAATGTCACTCGAAGAGAAATGGGAAATAGAAACATTTCCA	3060
Db	3120	GA AAAA CTTTGAGGAACATTTCAATGTCACTCGAAGAGAAATGGGAAATAGAAACATTTCCA	3179
Qy	3061	AGTACAGTGAGCAAAATAGCCGCTAAATAAATAGAGAAATGTTTTAAAGGAGCCAGC	3120
Db	3180	AGTACAGTGAGCAAAATAGCCGCTAAATAAATAGAGAAATGTTTTAAAGGAGCCAGC	3239
Qy	3121	TCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCGAGTATTAATGAA	3180
Db	3240	TCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCGAGTATTAATGAA	3299
Qy	3181	ATAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTGTGTGAACACAGAGGCCAAATTTG	3240
Db	3300	ATAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTGTGTGAACACAGAGGCCAAATTTG	3359
Qy	3241	AATGCTATGCTTAGATTAGGGGTTTTGCCAACTCAGGCTCTATAACAAAGTCTTCTCTGGA	3300
Db	3360	AATGCTATGCTTAGATTAGGGGTTTTGCCAACTCAGGCTCTATAACAAAGTCTTCTCTGGA	3419
Qy	3301	AGTAATTTCTAAGCACTCTGAAAATAAAAAGCAGAAATATGAAGTAGTTCAGACTGTT	3360
Db	3420	AGTAATTTCTAAGCACTCTGAAAATAAAAAGCAGAAATATGAAGTAGTTCAGACTGTT	3479
Qy	3361	AATACAGATTTCTCTCCATATCTGATTTCCAGATAAATAGAAACAGCCTATGGGAAAGTAGT	3420
Db	3480	AATACAGATTTCTCTCCATATCTGATTTCCAGATAAATAGAAACAGCCTATGGGAAAGTAGT	3539
Qy	3421	CATGCATCTCAGGTTTGTCTGAGACACCTGGA TGA CCGTGTAGATGATGTGAAATAAAG	3480
Db	3540	CATGCATCTCAGGTTTGTCTGAGACACCTGGA TGA CCGTGTAGATGATGTGAAATAAAG	3599
Qy	3481	GAAGATACTAGTTTGTCTGAAAATGACATTAAGGAAGTTCTGCTGTTTTTATGCAAAAGC	3540
Db	3600	GAAGATACTAGTTTGTCTGAAAATGACATTAAGGAAGTTCTGCTGTTTTTATGCAAAAGC	3659
Qy	3541	GTCCAGAGAGGAGCTTAGCAGGAGTCTTAGGCCCTTTCCACCATACACATTTGGCTCAG	3600
Db	3660	GTCCAGAGAGGAGCTTAGCAGGAGTCTTAGGCCCTTTCCACCATACACATTTGGCTCAG	3719
Qy	3601	GGTTACCGAAGAGGGGCCAAGAAATTAGCTGCTCAGAGAGAACTTATCTAGTAGGAT	3660
Db	3720	GGTTACCGAAGAGGGGCCAAGAAATTAGCTGCTCAGAGAGAACTTATCTAGTAGGAT	3779
Qy	3661	GAAGAGCTTCCCTGCTTCCAAACCTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3720
Db	3780	GAAGAGCTTCCCTGCTTCCAAACCTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3839
Qy	3721	TCTACTAGGATATAGCACCGTTGTCTACCGAGTGTCTGTCTAAGAAACACAGAGGAGAAATTTA	3780
Db	3840	TCTACTAGGATATAGCACCGTTGTCTACCGAGTGTCTGTCTAAGAAACACAGAGGAGAAATTTA	3899
Qy	3781	TTATCATTTGAAGAAATAGCTTTAAATGACTCGAGTAAACCAAGTAAATATTTGGCAAAAGGCATCT	3840
Db	3900	TTATCATTTGAAGAAATAGCTTTAAATGACTCGAGTAAACCAAGTAAATATTTGGCAAAAGGCATCT	3959
Qy	3841	CAGGAACATCACCTTAGTGAGGAACAAAAATTTCTGCTAGCTTGTTTCTTCCACAGTGC	3900
Db	3960	CAGGAACATCACCTTAGTGAGGAACAAAAATTTCTGCTAGCTTGTTTCTTCCACAGTGC	4019

QY 4981 GAAATTTATGCTCGTGACAGTTGTCAGAGAAACACACATCACTTTAACTAACTTAATT 5040
Db 5100 GAAATTTATGCTCGTGACAGTTGTCAGAGAAACACACATCACTTTAACTTAATT 5159
QY 5041 ACTCAAGAGACTACTCAATGTTGTTATGAAGACAGATGCTGAGTTGTGTGACGAC 5100
Db 5160 ACTCAAGAGACTACTCAATGTTGTTATGAAGACAGATGCTGAGTTGTGTGACGAC 5219
QY 5101 CTGAAATATTTCTAGCAATTCGGGAGGAAATGGGTAGTTAGTCTATTTCTGGTGACC 5160
Db 5220 CTGAAATATTTCTAGCAATTCGGGAGGAAATGGGTAGTTAGTCTATTTCTGGTGACC 5279
QY 5161 CAGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTG 5220
Db 5280 CAGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTG 5339
QY 5221 GTCAATGGAAGAACACCAAGGTCCTCAAGCGACAGAGAAATCCAGGACAGAAATGC 5280
Db 5340 GTCAATGGAAGAACACCAAGGTCCTCAAGCGACAGAGAAATCCAGGACAGAAATGC 5399
QY 5281 TTCAGGGGGCTAGAAATCTGTTGTTATGAGGCGCTTCAACCAATGCCCACAGATCAACTG 5340
Db 5400 TTCAGGGGGCTAGAAATCTGTTGTTATGAGGCGCTTCAACCAATGCCCACAGATCAACTG 5459
QY 5341 GAATGATGTGTACAGCTGTGTGCTGCTCTGCTGCTGAGAGCTTTCATCATCACTT 5400
Db 5460 GAATGATGTGTACAGCTGTGTGCTGCTCTGCTGCTGAGAGCTTTCATCATCACTT 5519
QY 5401 GGCAAGGTGTCCACCAATGTTGTTGTCAGGCGCATGCTGGAAGAGGACATGGC 5460
Db 5520 GGCAAGGTGTCCACCAATGTTGTTGTCAGGCGCATGCTGGAAGAGGACATGGC 5579
QY 5461 TTCATGCAATGGGAGAGATGTGTAGGCGACCTGTGTGACCGAGAGTGGTGTGGAC 5520
Db 5580 TTCATGCAATGGGAGAGATGTGTAGGCGACCTGTGTGACCGAGAGTGGTGTGGAC 5639
QY 5521 AGTGTAGCACTTACCAAGTGTGAGGAGCTGACACCTTACCTGATACCCAGATCCGCCAC 5580
Db 5640 AGTGTAGCACTTACCAAGTGTGAGGAGCTGACACCTTACCTGATACCCAGATCCGCCAC 5699
QY 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708
RESULT 13
AAAT87085
ID AAAT87085 standard; cDNA, 5711 BP.
AC AAAT87085;
XX
DT 06-JAN-1998 (first entry)
XX
DE Human BRCA1 gene consensus.
XX
KW BRCA1 gene; BRCA1(omi); breast cancer; ovary cancer; polymorphism;
XX genetic testing; diagnosis; gene therapy; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 120..5711
FT /*tag= a
FT 2201
FT variation /*tag= b
FT /*note= "AGC (40%) and AGT (55-65%) polymorphism at
FT position 2201"
FT 2430
FT variation /*tag= c
FT /*note= "35-45% TTG (Leu) and 55-65% CTG (Leu)
FT polymorphism at position 2430"
FT 2731
FT variation /*tag= d

FT variation /note= "25-35% CCG (Pro) and 65-75% CTG (Leu)
FT polymorphism at position 2731"
FT 3232
FT /*tag= e
FT /note= "35-45% GAA (Glu) and 55-65% GGA (Gly)
FT polymorphism at position 3232"
FT 3667
FT /*tag= f
FT /note= "35-45% AAA (Lys) and 55-65% AGA (Arg)
FT polymorphism at position 3667"
FT 4427
FT /*tag= g
FT /note= "45-55% TCT (Ser) and 45-55% TCC (Ser)
FT polymorphism at position 4427"
FT 4956
FT /*tag= h
FT /note= "35-45% AGT (Ser) and 55-65% GGT (Gly)
FT polymorphism at position 4956"
PN US5654155-A.
XX
XX 05-AUG-1997.
XX
XX 12-FEB-1996; 96US-00598591.
XX
XX 12-FEB-1996; 96US-00598591.
PR
XX {ONCO-} ONCORMED INC.
XX
XX Olson SJ, Allen AC, Zeng B, Schelter DB, Alvares CP, Murphy PD;
PI Critz BS;
XX
DR WPI; 1997-401843/37.
DR P-PSDB; AAW26522.
XX
PT Human BRCA1 gene coding sequence with common normal polymorphisms - for
XX assessing susceptibility to breast or ovarian cancer.
XX
PS Claim 1; Col 19-24; 35pp; English.
XX
CC This nucleotide sequence comprises a consensus DNA sequence, designated
CC BRCA1(omi), for the normal human BRCA1 gene. It was found by end-to-end
CC sequencing of the BRCA1 gene from 5 individuals randomly drawn from the
CC population and found to have no family history of breast or ovarian
CC cancer. The BRCA1(omi) gene and the seven polymorphic sites (which are
CC not associated with breast or ovarian cancer) will provide greater
CC accuracy and reliability for genetic testing. A claimed method for
CC detecting an increased genetic susceptibility to breast and ovarian
CC cancer resulting from the presence of a mutation in the BRCA1 coding
CC sequence involves amplifying and sequencing the BRCA1 coding sequence
CC from an individual and comparing the sequence with BRCA1(omi). The
CC consensus normal BRCA1 sequence can also be used in gene therapy, to make
CC diagnostic probes and to express normal BRCA1 polypeptide (see AAW26522).
XX
SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;

Query Match 100.0%; Score 5587.4; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGATTATCTGCTCTCGCGTTGAAGAGTACAAATGTCATTATGCTATGAGAAA 60
Db 120 ATGGATTATCTGCTCTCGCGTTGAAGAGTACAAATGTCATTATGCTATGAGAAA 179
QY 61 ATCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACTGTCTCCACAAGTGTGAC 120
Db 180 ATCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACTGTCTCCACAAGTGTGAC 239
QY 121 CACATATTTGCAAAATTTTGGATGCTGAACTTCTCAACAGAGAAAGGGCTTCACAG 180
Db 240 CACATATTTGCAAAATTTTGGATGCTGAACTTCTCAACAGAGAAAGGGCTTCACAG 299
QY 181 TGTCTTTTATGTAGAGATGATATACCAAAAGGAGCTCACAGAAAGTACGAGATTAGT 240

QY 2401 TGTGTGAGTCAGTGTGACAGATTTGAAACCCCAAGGAGCTAAATTCATGTTGTTGTTCCAAA 2460
DB 2520 TGTGTGAGTCAGTGTGACAGATTTGAAACCCCAAGGAGCTAAATTCATGTTGTTGTTCCAAA 2579
QY 2461 GATTAATAGAAATGACACAGAAAGGCTTTTAAGTATTCATTTGGGACATGAAGTTAAACACAGT 2520
DB 2580 GATTAATAGAAATGACACAGAAAGGCTTTTAAGTATTCATTTGGGACATGAAGTTAAACACAGT 2639
QY 2521 CGGGAAACACATAGAAATCGGAAGAGTGAACCTTGATGCTCAGTATTTGCGAATATCA 2580
DB 2640 CGGGAAACACATAGAAATCGGAAGAGTGAACCTTGATGCTCAGTATTTGCGAATATCA 2699
QY 2581 TTCAAGGTTTCAAGCGCCAGTCATTTGCTCTGTTTCAATCCAGGAAATGCGAAGAG 2640
DB 2700 TTCAAGGTTTCAAGCGCCAGTCATTTGCTCTGTTTCAATCCAGGAAATGCGAAGAG 2759
QY 2641 GAATGTCACATTTCTGCGCCACCTCTGGGTCCTTAAGAAACCAAGTCCAAAGTCACT 2700
DB 2760 GAATGTCACATTTCTGCGCCACCTCTGGGTCCTTTAAGAAACCAAGTCCAAAGTCACT 2819
QY 2701 TTTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCCTGTA 2760
DB 2820 TTTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCCTGTA 2879
QY 2761 CAGACAGTTAATATCACTGACAGGCTTTCTGCTGGTGGTCAAGAAAGATGACCCAGTTGAT 2820
DB 2880 CAGACAGTTAATATCACTGACAGGCTTTCTGCTGGTGGTCAAGAAAGATGACCCAGTTGAT 2939
QY 2821 AATGCCAAATGTAGTATCAAGAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGGC 2880
DB 2940 AATGCCAAATGTAGTATCAAGAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGGC 2999
QY 2881 AACGAACTGACATCACTCTCCTCAATTAACATGACCTTTTACAAAACCCATATCGTATA 2940
DB 3000 AACGAACTGACATCACTCTCCTCAATTAACATGACCTTTTACAAAACCCATATCGTATA 3059
QY 2941 CCACACATTTTCCCATCACTGACATTTGTTTAAACTAAATGTAAGAAATCTGCTAGAG 3000
DB 3060 CCACACATTTTCCCATCACTGACATTTGTTTAAACTAAATGTAAGAAATCTGCTAGAG 3119
QY 3001 GAAACCTTTGAGGAACATTTCAATGTCACTGACCTGAAGAGAAATGGGAAATGAGAACTTCCA 3060
DB 3120 GAAACCTTTGAGGAACATTTCAATGTCACTGACCTGAAGAGAAATGGGAAATGAGAACTTCCA 3179
QY 3061 AGTACAGTGACACATTTAGCCGTAATAACATTAAGAGAAATGTTTTAAAGGAGCCAGC 3120
DB 3180 AGTACAGTGACACATTTAGCCGTAATAACATTAAGAGAAATGTTTTAAAGGAGCCAGC 3239
QY 3121 TCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3180
DB 3240 TCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3299
QY 3181 ATAGTTCCAGTGATGAACATTTCAAGCAGAACTAGGTAGAACAGAGGCGCCAAATTC 3240
DB 3300 ATAGTTCCAGTGATGAACATTTCAAGCAGAACTAGGTAGAACAGAGGCGCCAAATTC 3359
QY 3241 AATGCTATGCTTAGATTTAGGGGTTTTCACCTGAGGCTCTATAAACAAAGTCTTCTCTGGA 3300
DB 3360 AATGCTATGCTTAGATTTAGGGGTTTTCACCTGAGGCTCTATAAACAAAGTCTTCTCTGGA 3419
QY 3301 AGTAATTTGAAGCATCTCTGAATTAAGGAAAGGCAAGATATGAAGAGTAGTTCAGACTGTT 3360
DB 3420 AGTAATTTGAAGCATCTCTGAATTAAGGAAAGGCAAGATATGAAGAGTAGTTCAGACTGTT 3479
QY 3361 AATAACAGATTTCTCTCCATATCTGATTTGAGATTAATTTAGAACAGGCTATGGGAAGTAGT 3420
DB 3480 AATAACAGATTTCTCTCCATATCTGATTTGAGATTAATTTAGAACAGGCTATGGGAAGTAGT 3539
QY 3421 CATGCACTCTCAGGTTTGTGTCAGACACCTGATGACCTGTTAGATGATGTTGAATTAAG 3480
DB 3540 CATGCACTCTCAGGTTTGTGTCAGACACCTGATGACCTGTTAGATGATGTTGAATTAAG 3599

QY 3481 GAAGATACTAGTTTCTGCTGAAATGACATTAAGGAAAGTCTGCTGTTTTTTAGCAAAAGC 3540
DB 3600 GAAGATACTAGTTTCTGCTGAAATGACATTAAGGAAAGTCTGCTGTTTTTTAGCAAAAGC 3659
QY 3541 GTCCAGAGGAGAGCTTTAGCAGAGTCTAGCCCTTTTCCACCATACATTTGGCTCAG 3600
DB 3660 GTCCAGAGGAGAGCTTTAGCAGAGTCTAGCCCTTTTCCACCATACATTTGGCTCAG 3719
QY 3601 GGTTCACCGAAGAGGGGCCCAAGAAATAGAGTCTCTCAGAAAGAGAACTTATCTAGTAGGAT 3660
DB 3720 GGTTCACCGAAGAGGGGCCCAAGAAATAGAGTCTCTCAGAAAGAGAACTTATCTAGTAGGAT 3779
QY 3661 GAAGAGCTTCCCTGCTTCCAACTTTGTTTGGTAAAGTAAACAAATATCTCTCAG 3720
DB 3780 GAAGAGCTTCCCTGCTTCCAACTTTGTTTGGTAAAGTAAACAAATATCTCTCAG 3839
QY 3721 TCTACTAGGATGACACCGTTGCTACCGAGTGTCTCTTAAGAAACACAGAGAGAAATTTA 3780
DB 3840 TCTACTAGGATGACACCGTTGCTACCGAGTGTCTCTTAAGAAACACAGAGAGAAATTTA 3899
QY 3781 TTATCATTTGAAGAAATAGCTTAAATGACTGAGTAACCAAGTAAATTTGGAAAGGATCT 3840
DB 3900 TTATCATTTGAAGAAATAGCTTAAATGACTGAGTAACCAAGTAAATTTGGAAAGGATCT 3959
QY 3841 CAGGAAACATCACCTTAGTGAGGAAACAAATGTTCTGTAGCTTGTCTTCTCACAGTGC 3900
DB 3960 CAGGAAACATCACCTTAGTGAGGAAACAAATGTTCTGTAGCTTGTCTTCTCACAGTGC 4019
QY 3901 AGTGAATTTGGAAGACTTTGACTGCAAAATCAAAACCAAGGATCTTCTTTGATTTGTTCT 3960
DB 4020 AGTGAATTTGGAAGACTTTGACTGCAAAATCAAAACCAAGGATCTTCTTTGATTTGTTCT 4079
QY 3961 TCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCACAGGAAATTC 4020
DB 4080 TCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCACAGGAAATTC 4139
QY 4021 GTTTCAGATGATGAAGAAAGAGGAAACGGCTTTGGAGAAATAATCAAGAGAGCAAAAGC 4080
DB 4140 GTTTCAGATGATGAAGAAAGAGGAAACGGCTTTGGAGAAATAATCAAGAGAGCAAAAGC 4199
QY 4081 ATGGATTTCAACTTAGTGAGCAGCATCTGGTGTGAGAGTGAACACAGCTCTCTGAA 4140
DB 4200 ATGGATTTCAACTTAGTGAGCAGCATCTGGTGTGAGAGTGAACACAGCTCTCTGAA 4259
QY 4141 GACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATG 4200
DB 4260 GACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATG 4319
QY 4201 CAACATAA CTTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAG 4260
DB 4320 CAACATAA CTTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAG 4379
QY 4261 CATGGAGCCAGCTTCTAACAGTACCTTCCATCATAAAGTACCTCTGCTGCTTGGAG 4320
DB 4380 CATGGAGCCAGCTTCTAACAGTACCTTCCATCATAAAGTACCTCTGCTGCTTGGAG 4439
QY 4321 GACCTCGGAAATCCAGAAACAAAGCAGCATCAGAAAAAGCAGTATTAATCTTCAAGAAAGT 4380
DB 4440 GACCTCGGAAATCCAGAAACAAAGCAGCATCAGAAAAAGCAGTATTAATCTTCAAGAAAGT 4499
QY 4381 AGTGAATCCCTTATAGCCAGAAATCAGAGGCTTTCTGCTCAGAAAGTTTGAAGGTTCT 4440
DB 4500 AGTGAATCCCTTATAGCCAGAAATCAGAGGCTTTCTGCTCAGAAAGTTTGAAGGTTCT 4559
QY 4441 GCAGATAGTCTTACCAAGTAAATAAAGAACACAGGAGTGGAAAGGTCATCCCTCTCTAAA 4500
DB 4560 GCAGATAGTCTTACCAAGTAAATAAAGAACACAGGAGTGGAAAGGTCATCCCTCTCTAAA 4619
QY 4501 TGGCCATCATTAAGATAGTGGTGTACATGCACTTGTCTCTGGAGTCTTTCAGATAGA 4560
DB 4620 TGGCCATCATTAAGATAGTGGTGTACATGCACTTGTCTCTGGAGTCTTTCAGATAGA 4679
QY 4561 AACTACCATCTCAAGAGGAGCTCTAATTAAGTGTGATGTTGAGAGGAGCAACAGCTGGAA 4620

Db 4680 AACTACCATCTCAAGAGGCTCAITTAAGGTGTGTATGTGAGGAGCAACAGCTGGAA 4739
QY 4621 GAGTCTGGCCACACGATTTGACCGAACAATCTTACTTTCGCAAGCGAAGATCTAGAGGA 4680
Db 4740 GAGTCTGGCCACACGATTTGACCGAACAATCTTACTTTCGCAAGCGAAGATCTAGAGGA 4799
QY 4681 ACCCTTTACCTGGAATCTGGAATCAGGCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT 4740
Db 4800 ACCCTTTACCTGGAATCTGGAATCAGGCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT 4859
QY 4741 GAAGACAGAGCCACAGATGAGCTGCTGTTGGCAACATACCATCTTCAACTCTGCAATG 4800
Db 4860 GAAGACAGAGCCACAGATGAGCTGCTGTTGGCAACATACCATCTTCAACTCTGCAATG 4919
QY 4801 AAGCTTCCCAATTTGAAGTTGACAGAAATCTGCCAGAGGTCCAGCTGCTGCTCATACTACT 4860
Db 4920 AAGTTCCTCCCAATTTGAAGTTGACAGAAATCTGCCAGAGGTCCAGCTGCTGCTCATACTACT 4979
QY 4861 GATCTCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGAGGACCAAGTTGACA 4920
Db 4980 GATCTCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGAGGACCAAGTTGACA 5039
QY 4921 GCTTCAACAGAGGGTCAACAAAGAAATGTCATGTTGCTGCTGCTGACCCACAGAA 4980
Db 5040 GCTTCAACAGAGGGTCAACAAAGAAATGTCATGTTGCTGCTGCTGACCCACAGAA 5099
QY 4981 GAATTTATGCTGCTGTAAGTTTGGCAGAAACACACATCATCTTTAACTTAATCTAAAT 5040
Db 5100 GAATTTATGCTGCTGTAAGTTTGGCAGAAACACACATCATCTTTAACTTAATCTAAAT 5159
QY 5041 ACTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTTGTTGAGCAGCA 5100
Db 5160 ACTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTTGTTGAGCAGCA 5219
QY 5101 CTGAATATTTCTAGGAATTCGCGAGGAGAAATGCGTAGTACTATTTCTGGGTGACC 5160
Db 5220 CTGAATATTTCTAGGAATTCGCGAGGAGAAATGCGTAGTACTATTTCTGGGTGACC 5279
QY 5161 CAGTCTATTAAGAGAGAAATGCTGAATGAGTGAATTTGAGTCAAGAGGAGATGCTG 5220
Db 5280 CAGTCTATTAAGAGAGAAATGCTGAATGAGTGAATTTGAGTCAAGAGGAGATGCTG 5339
QY 5221 GTCATGGAAGAAACCAAGGTCACAAAGGAGCAAGAGAAATCCCAAGGACAGAAAGATC 5280
Db 5340 GTCATGGAAGAAACCAAGGTCACAAAGGAGCAAGAGAAATCCCAAGGACAGAAAGATC 5399
QY 5281 TTGAGGGGCTAGAAATCTGTTGCTATGAGGCTTACCAACATGCGCCACAGATCAACTG 5340
Db 5400 TTGAGGGGCTAGAAATCTGTTGCTATGAGGCTTACCAACATGCGCCACAGATCAACTG 5459
QY 5341 GAATGATGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5400
Db 5460 GAATGATGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5519
QY 5401 GGCAAGGTGTCCACCCCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5460
Db 5520 GGCAAGGTGTCCACCCCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5579
QY 5461 TTCCATGCAATTTGGGCAAGTGTGAGGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5520
Db 5580 TTCCATGCAATTTGGGCAAGTGTGAGGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5639
QY 5521 AGTGTAGCTCTACCAAGTCCAGGAGCTGAGACCTTACCTGATACCCACAGATCCCCAC 5580
Db 5640 AGTGTAGCTCTACCAAGTCCAGGAGCTGAGACCTTACCTGATACCCACAGATCCCCAC 5699
QY 5581 AGCAGCTAC 5589
Db 5700 AGCAGCTAC 5708

RESULT 14

AAV46448
ID AAV46448 standard; cDNA; 5711 BP.
XX
AC AAV46448;
XX
DT 18-NOV-1998 (first entry)
XX
DE Human BRCA1 omil cDNA.
XX
KW BRCA1; omil; human; breast and ovarian cancer predisposing gene;
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT /tag= a
FT /product= "BRCA1 omil protein"
XX
XX US5750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-00798691.
XX
XX 12-FEB-1996; 96US-00598591.
XX
XX (ONCO-) ONCORMED INC.
XX
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
XX Critz BS;
XX
XX WPI; 1998-296774/26.
XX P-PSDB; AAW76098.
XX
XX BRCA1 omil gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.
XX
XX Claim 2d; Col 27-32; 54pp; English.
XX
XX This sequence encodes the human BRCA1 (breast and ovarian cancer
XX predisposing gene) omil gene. This sequence and polymorphic variations of
XX this sequence are useful for the identification of an individual who may
XX or may not have an increased susceptibility to breast or ovarian cancer.
XX The sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome 17q
XX which is known to be linked to cancer susceptibility, especially breast
XX cancer. Cells containing a mutation in this gene lose the wild-type
XX function of BRCA1 and are more susceptible to cancers
XX
XX Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;
XX

Query Match 100.0%; Score 5587.4; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGATTATCTGCTTCGCTTGGAGTGTGATCAAGAACTGCTATGCTATGCGAGAA 60
Db 120 ATGGAATTTATCTGCTTCGCTTGGAGTGTGATCAAGAACTGCTATGCTATGCGAGAA 179
QY 61 ATCTTAGAGTGTCCCATCTGCTGAGAGTGTGATCAAGAACTGCTTCACAAAGTGTGAC 120
Db 180 ATCTTAGAGTGTCCCATCTGCTGAGAGTGTGATCAAGAACTGCTTCACAAAGTGTGAC 239
QY 121 CACATATTTTGCATAATTTTGCATGCTGAACCTTCTCAACAGAGAAAGGCGCTTCACAG 180
Db 240 CACATATTTTGCATAATTTTGCATGCTGAACCTTCTCAACAGAGAAAGGCGCTTCACAG 299
QY 181 TGTCTTTATGTAAGATGATATACCAAAAGAGCGCTTACAAGAAAGTACGAGATTTAGT 240

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300 TGTCTTTATGTAGATGATATATACCAAAAGAGCCCTACAGAAAGTACAGGATTTAGT 359
241 CAACCTGTGTGAAGAGCTATTGAAATCATTTTGTCTTTTCAGCTTTGACACAGGTTTGAG 300
360 CAACCTGTGTGAAGAGCTATTGAAATCATTTTGTCTTTTCAGCTTTGACACAGGTTTGAG 419
301 TATCGAACACGCTATATTTTGCAGAAAGGAAATATCTCTCTGACACATCTAARAGAT 360
420 TATGCAAAACGCTATATTTTGCAGAAAGGAAATATCTCTCTGACACATCTAARAGAT 479
361 GAAGTTTCTATCATCTCAAAAGTATGGCTACAGAAACCGTGCAGAAAGCTTTCTACAGAGT 420
480 GAAGTTTCTATCATCTCAAAAGTATGGCTACAGAAACCGTGCAGAAAGCTTTCTACAGAGT 539
421 GAACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 480
540 GAACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 599
481 ACTGTGAGAACTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 540
600 ACTGTGAGAACTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 659
541 GAATTTGGATCTGATCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 600
660 GAATTTGGATCTGATCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 719
601 GATCAAGATTTGTACAAATCAACCCCTCAAGCAACAGGATGAAATCAGTTTGGATTCT 660
720 GATCAAGATTTGTACAAATCAACCCCTCAAGCAACAGGATGAAATCAGTTTGGATTCT 779
661 GCAAAAAGGCTGTCTGTGAAATTTTCTGAGCGGATGATCAAAATCTGAAATCATCAA 720
780 GCAAAAAGGCTGTCTGTGAAATTTTCTGAGCGGATGATCAAAATCTGAAATCATCAA 839
721 CCCAGTAAATGATTTGAAACCACTGAGAGCGGTGAGTGAAGGCAATCCAGAAAG 780
840 CCCAGTAAATGATTTGAAACCACTGAGAGCGGTGAGTGAAGGCAATCCAGAAAG 899
781 TATCAGGATAGTCTGTGTTTCAAACTTGATGTGAGCGCATGTGCGCAAAATCTCATGCC 840
900 TATCAGGATAGTCTGTGTTTCAAACTTGATGTGAGCGCATGTGCGCAAAATCTCATGCC 959
841 AGCTCATTTACAGCATGAGAACAGCAGTTTATCTCACTAAGACAGATGATGTAGAA 900
960 AGCTCATTTACAGCATGAGAACAGCAGTTTATCTCACTAAGACAGATGATGTAGAA 1019
901 AAGGCTGAAATTTCTGTAATAAAGCAAAACAGCTGGCTTAGCAGAGCCCAACATAACAGA 960
1020 AAGGCTGAAATTTCTGTAATAAAGCAAAACAGCTGGCTTAGCAGAGCCCAACATAACAGA 1079
961 TGGGCTGGAAGTAAAGGAAACATGTAAATGATAGGCGGACTCCAGCACAGAAAGGTA 1020
1080 TGGGCTGGAAGTAAAGGAAACATGTAAATGATAGGCGGACTCCAGCACAGAAAGGTA 1139
1021 GATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGC 1080
1140 GATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGC 1199
1081 TCAGAGAACTCTAGAGATACTGAAGATGTTCTTGGATTAACATAAATAGCAGAACTTCAG 1140
1200 TCAGAGAACTCTAGAGATACTGAAGATGTTCTTGGATTAACATAAATAGCAGAACTTCAG 1259
1141 AAAGTTAATCAGTGTGTTTCCAGAAAGTATCACTGTTAGTGTCTGATGATCTCAGATGAT 1200
1260 AAAGTTAATCAGTGTGTTTCCAGAAAGTATCACTGTTAGTGTCTGATGATCTCAGATGAT 1319
1201 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTTGAGCGTTCTTAAATAGAGGTAGAT 1260
1320 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTTGAGCGTTCTTAAATAGAGGTAGAT 1379
1261 GAATATCTGCTCTTTCAGACAAATAGATCTTACCTGGCCAGTGTCTCTATGAGGCTTTA 1320
|||||

1380 GAATATCTGCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGTCTCTCATGAGGCTTTA 1439
1321 ATATGTAAAGTGAAGAGTTCTCTCAAAATCAGTGTAGAGTAATATTTGAGAGCAAAATA 1380
1440 ATATGTAAAGTGAAGAGTTCTCTCAAAATCAGTGTAGAGTAATATTTGAGAGCAAAATA 1499
1381 TTTGGGAAACCTTATCGGAAAGGCAAGCTCCCAACTTTAAGCCATGTAACTGAAAT 1440
1500 TTTGGGAAACCTTATCGGAAAGGCAAGCTCCCAACTTTAAGCCATGTAACTGAAAT 1559
1441 CTAAATATAGGAGCATTTGTACTGAGCCACAGATTAATCAAGAGCGTCCCTCTCAAAAT 1500
1560 CTAAATATAGGAGCATTTGTACTGAGCCACAGATTAATCAAGAGCGTCCCTCTCAAAAT 1619
1501 AAATTAAGCGTGAAGAGGACCTCATCAGGCTCTTCACTCTGAGATTTTATCAAGAA 1560
1620 AAATTAAGCGTGAAGAGGACCTCATCAGGCTCTTCACTCTGAGATTTTATCAAGAA 1679
1561 GCAGATTTGGCAGTTTCAAAAGACCTCTGAAATGATAAATCAGGAACTAAACCAACGGAG 1620
1680 GCAGATTTGGCAGTTTCAAAAGACCTCTGAAATGATAAATCAGGAACTAAACCAACGGAG 1739
1621 CAGATGTCTCAGTGTGATTAATTAATAGTGTCTATGAGTAATTAACCAACGGAGTAT 1680
1740 CAGATGTCTCAGTGTGATTAATTAATAGTGTCTATGAGTAATTAACCAACGGAGTAT 1799
1681 TCTATTCAAGATCAGAGAAATCTTAACCCCAATAGAAATCACTCGAAAGAAATCTGCTTTT 1740
1800 TCTATTCAAGATCAGAGAAATCTTAACCCCAATAGAAATCACTCGAAAGAAATCTGCTTTT 1859
1741 AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCTGAAATTAATATC 1800
1860 AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCTGAAATTAATATC 1919
1801 CACAAATCAAAAGCACCTTAAAGAAATAGCTGTAGGAGAGTCTTCTACAGGCAATAT 1860
1920 CACAAATCAAAAGCACCTTAAAGAAATAGCTGTAGGAGAGTCTTCTACAGGCAATAT 1979
1861 CATGCTTTGAACCTAGTGTAGTGTAGTGTAAAGCCCACTTAATTTGTACTGAAATTCGAA 1920
1980 CATGCTTTGAACCTAGTGTAGTGTAGTGTAAAGCCCACTTAATTTGTACTGAAATTCGAA 2039
1921 ATTGTATAGTTGTCTAGCAGTGAAGAGATAAGAAAAAAGTACAAACCAATTCGCAATC 1980
2040 ATTGTATAGTTGTCTAGCAGTGAAGAGATAAGAAAAAAGTACAAACCAATTCGCAATC 2099
1981 AGGCACAGCAGAAACCTTCAACTCATGAGGTAAAGAACTTGCACCTCGAGCCAGAGAG 2040
2100 AGGCACAGCAGAAACCTTCAACTCATGAGGTAAAGAACTTGCACCTCGAGCCAGAGAG 2159
2041 AGTAACAGCCCAATGAAACAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2100
2160 AGTAACAGCCCAATGAAACAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2219
2101 AAGTTAAACAAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACCACTGTAACCTTAAAGAA 2160
2220 AAGTTAAACAAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACCACTGTAACCTTAAAGAA 2279
2161 TTTGTCAATCTCTAGCTTCCAGAGAGAGAAAGAGAGAACTAGAAACAGTAAAGT 2220
2280 TTTGTCAATCTCTAGCTTCCAGAGAGAGAAAGAGAGAACTAGAAACAGTAAAGT 2339
2221 TCTAATATGCTGAGAGCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAAACT 2280
2340 TCTAATATGCTGAGAGCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAAACT 2399
2281 GAAAGATCTGTAGAGTAGCAGTATTTCACTGTTACTGTTACTGTTATTTGGCACTCAG 2340
2400 GAAAGATCTGTAGAGTAGCAGTATTTCACTGTTACTGTTACTGTTATTTGGCACTCAG 2459
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2460 GAAAGTATCTCTCTACTGGAAGTGTAGCTCTCTAGGGAAGGCAAAACAGAAACCAATTA 2519

QY 2401 TGTGTAGTCAAGTGTGAGCAATTTGAAACCCCAAGGACTAATTCATGTGTGTTCCAAA 2460
DB TGTGTAGTCAAGTGTGAGCAATTTGAAACCCCAAGGACTAATTCATGTGTGTTCCAAA 2579
QY 2461 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGT 2520
DB GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGT 2639
QY 2521 CGGAAACAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACA 2580
DB CGGAAACAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACA 2699
QY 2581 TTCAAGGTTTCAAGGCGCAGTCAATTTGCTGCTGTTTCAATCCAGGAAATGCAAGAGAG 2640
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QY 2701 TTTGAATGTGAACAAAGGAGAAATCAAGGAAAGTGAATGCTAATATCAAGCCCTGTA 2760
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QY 2761 CAGACAGTAAATATCACTGAGGCTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
DB CAGACAGTAAATATCACTGAGGCTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2939
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DB AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAGAGGC 2999
QY 2881 AACGAACTCGACTCATTTACTCCAAATAAATCATGACCTTTTACAAACCCATATCGTATA 2940
DB AACGAACTCGACTCATTTACTCCAAATAAATCATGACCTTTTACAAACCCATATCGTATA 3059
QY 2941 CCACCACTTTTCCATCAAGTCAATTTGTTTAAACTAAATGTAGAGAAATCTCTAGAG 3000
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QY 3001 GAAAACTTTGAGGAACTCAATGCTACCTGGAAGAGAAATGGAATGGAATGGAATGGAATGGA 3060
DB GAAAACTTTGAGGAACTCAATGCTACCTGGAAGAGAAATGGAATGGAATGGAATGGAATGGA 3179
QY 3061 AGTACAGTGAAGCAATTTAGCCGTAATACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3120
DB AGTACAGTGAAGCAATTTAGCCGTAATACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3239
QY 3121 TCAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAGTGGCTCCAGTATTAATGAA 3180
DB TCAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAGTGGCTCCAGTATTAATGAA 3299
QY 3181 ATAGGTTTCCAGTGAATGAAACATTTCAAGCAGAACTAGTAGAAACAGAGGCGCCAAATTTG 3240
DB ATAGGTTTCCAGTGAATGAAACATTTCAAGCAGAACTAGTAGAAACAGAGGCGCCAAATTTG 3359
QY 3241 AATGCTATGCTTAGATTAGGGTTTGGCAACCTGAGTCTATTAACAAAGTCTTCTCTGGA 3300
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QY 3301 AGTAAATGTAAGCATCTCTGAAATATAAAGCAAGAAATATGAAGAGTGTTCAGACTGTT 3360
DB AGTAAATGTAAGCATCTCTGAAATATAAAGCAAGAAATATGAAGAGTGTTCAGACTGTT 3479
QY 3361 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTTAGAAACAGCTATGGAAGTACT 3420
DB AATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTTAGAAACAGCTATGGAAGTACT 3539
QY 3421 CATGCCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGCTGGAATAGAG 3480
DB CATGCCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGCTGGAATAGAG 3599

QY 3481 GAAGATATCTAGTGTGCTGAAATATGACATTAAGGAAAGTTTCTGCTGTCTTTTACGAAAAGC 3540
DB GAAGATATCTAGTGTGCTGAAATATGACATTAAGGAAAGTTTCTGCTGTCTTTTACGAAAAGC 3659
QY 3541 GTCCAGAGAGGAGCTTACAGAGGCTTCTAGCCCTTTTACCCATACACATTTGGCTCAG 3600
DB GTCCAGAGAGGAGCTTACAGAGGCTTCTAGCCCTTTTACCCATACACATTTGGCTCAG 3719
QY 3601 GGTTCACGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGGAT 3660
DB GGTTCACGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGGAT 3779
QY 3661 GAAGAGCTTCCCTGCTTCCAAACACTTGTATTTTGTAAAGTAAACATATACCTCTCAG 3720
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QY 3721 TCTATAGGCATAGCACCGTGTCTACCGAGTGTCTCTCTAAGAACACAGAGGAGAAATTTA 3780
DB TCTATAGGCATAGCACCGTGTCTACCGAGTGTCTCTCTAAGAACACAGAGGAGAAATTTA 3899
QY 3781 TTATCATTTGAGAAATAGCTTAAATGACTGCTACCAAGTATATTTGGCAAGGCTCT 3840
DB TTATCATTTGAGAAATAGCTTAAATGACTGCTACCAAGTATATTTGGCAAGGCTCT 3959
QY 3841 CAGGAAACATCCTTAGTGAAGAAACAAATGTTCTGTAGTGTGTTTCTTCAAGTGC 3900
DB CAGGAAACATCCTTAGTGAAGAAACAAATGTTCTGTAGTGTGTTTCTTCAAGTGC 4019
QY 3901 AGTGAATTTGAGAGCTTGTGCAATATACAAACACCCAGATCTCTTTCTTGTGTTCT 3960
DB AGTGAATTTGAGAGCTTGTGCAATATACAAACACCCAGATCTCTTTCTTGTGTTCT 4079
QY 3961 TCCAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGTGTGCTGAGTGCACAGGAAATTTG 4020
DB TCCAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGTGTGCTGAGTGCACAGGAAATTTG 4139
QY 4021 GTTTCAGATGATGAAGAAAGAGAAACCGGCTTTGGAAGAAATTAATCAAGAGGCAAGC 4080
DB GTTTCAGATGATGAAGAAAGAGAAACCGGCTTTGGAAGAAATTAATCAAGAGGCAAGC 4199
QY 4081 ATGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGGTGAAGAAACAGCGTCTCTGAA 4140
DB ATGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGGTGAAGAAACAGCGTCTCTGAA 4259
QY 4141 GACTGCTCAGGCTATCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGATACCATG 4200
DB GACTGCTCAGGCTATCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGATACCATG 4319
QY 4201 CAACATACCTGATTAAGCTCCAGAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAG 4260
DB CAACATACCTGATTAAGCTCCAGAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAG 4379
QY 4261 CATGGAGCCAGCTTCTTAACAGCTACCTTCCATCATTAAGTGAATCTTCCGCTTGGAG 4320
DB CATGGAGCCAGCTTCTTAACAGCTACCTTCCATCATTAAGTGAATCTTCCGCTTGGAG 4439
QY 4321 GACTGCGGAATTCAGAAACAAAGCAGCATCAGAAAAGCAGTATTAATCTCAGAGAAAGT 4380
DB GACTGCGGAATTCAGAAACAAAGCAGCATCAGAAAAGCAGTATTAATCTCAGAGAAAGT 4499
QY 4381 AGTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGCAAGTGTTCAGGTTGCT 4440
DB AGTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGCAAGTGTTCAGGTTGCT 4559
QY 4441 GCAGATAGTCTTACAGTAAAAATTAAGAAACAGAGGTGGAAGTCAATCCCTTCTAAA 4500
DB GCAGATAGTCTTACAGTAAAAATTAAGAAACAGAGGTGGAAGTCAATCCCTTCTAAA 4619
QY 4501 TCCCACTCATATAGATGATAGGTGATCATGACAGTCTGCTGGGAGTCTTTCAGATAGA 4560
DB TCCCACTCATATAGATGATAGGTGATCATGACAGTCTGCTGGGAGTCTTTCAGATAGA 4679
QY 4561 AACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGAGGAGCAACAGCTGGAA 4620

Db	4680		AACTACCCATCTCAAGAGGAGCTCATTAAGGTGTTGATGTGGAGGAGCAACAGCTGGAA	4739
Qy	4621	GAGTCTGGGCCACACGATTTTGACCGAAACATCTTACTTTGCGCAAGCCAGAGATCTAGAGGGA	4680	
Db	4740	GAGTCTGGGCCACACGATTTTGACCGAAACATCTTACTTTGCGCAAGCCAGAGATCTAGAGGGA	4799	
Qy	4681	ACCCCTTACCTGGAAATCTGGAAATCAGGCTCTTCTCTGATGACCCCTGAATCTGATCTCTTCT	4740	
Db	4800	ACCCCTTACCTGGAAATCTGGAAATCAGGCTCTTCTCTGATGACCCCTGAATCTGATCTCTTCT	4859	
Qy	4741	GAAGACAGAGGCCCCAGAGTCTGAGTCTGCTGTTGGCAACATACCATCTTCAAACCTCTGCATG	4800	
Db	4860	GAAGACAGAGGCCCCAGAGTCTGAGTCTGCTGTTGGCAACATACCATCTTCAAACCTCTGCATG	4919	
Qy	4801	AAAGTTTCCCAATTTGAAAGTTGCAAGATCTGCCCGAGGGTCAGCTGCTGCTCATCTACT	4860	
Db	4920	AAAGTTTCCCAATTTGAAAGTTTGCAGAAATCTGCCCGAGGGTCAGCTGCTGCTCATCTACT	4979	
Qy	4861	GATACTCTGGGTATATATGCAATGGAAAGAAAGTCTGAGCAGGGAGAAAGCCAGAAATTGACA	4920	
Db	4980	GATACTCTGGGTATATATGCAATGGAAAGAAAGTCTGAGCAGGGAGAAAGCCAGAAATTGACA	5039	
Qy	4921	GCTTCAACAGAAAGGGTCAACAAAGAAAGATGTCCATGTGTGTGTCTGGCTGTGAACCCAGAA	4980	
Db	5040	GCTTCAACAGAAAGGGTCAACAAAGAAAGATGTCCATGTGTGTGTCTGGCTGTGAACCCAGAA	5099	
Qy	4981	GAAATTTATGCTGTGTGTAACAAGTTTGCAGAAAAACACACATCACCTTTAACTAATCTAATT	5040	
Db	5100	GAAATTTATGCTGTGTGTAACAAGTTTGCAGAAAAACACACATCACCTTTAACTAATCTAATT	5159	
Qy	5041	ACTGAAGAGACTACTCATGTTGTTTATGAAAAACAGATCTGAGTTTGTGTGTGAACCGACA	5100	
Db	5160	ACTGAAGAGACTACTCATGTTGTTTATGAAAAACAGATCTGAGTTTGTGTGTGAACCGACA	5219	
Qy	5101	CTGAAATATTTTCTAGCAATGTCGGGAGGAAATGGCTAGTTAGCTATTTTCTGGGTGACC	5160	
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Qy	5221	GTCAATGGAGAAACCAACCAAGTTCCAAGCGAGCAAGAAATCCCAAGGACAGAAAGATC	5280	
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Qy	5281	TTCAAGGGGCTAGAAATCTGTGTCTATGGGCCCTTTCACCAACATGCCGCCACAGATCAACTG	5340	
Db	5400	TTCAAGGGGCTAGAAATCTGTGTCTATGGGCCCTTTCACCAACATGCCGCCACAGATCAACTG	5459	
Qy	5341	GAATGGATGTGACAGCTGTGTGTGTCTTGTGTGTGAAGAGCTTTCATCATTCACCCCTT	5400	
Db	5460	GAATGGATGTGACAGCTGTGTGTGTCTTGTGTGTGAAGAGCTTTCATCATTCACCCCTT	5519	
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Db	5520	GGCACAGGTGTCCACCCCAATTTGTTGTGTGTGCAGCCAGATGCTGTGACAGAGGACAAATGGC	5579	
Qy	5461	TTCCATGGAAATTTGGGCAAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGAC	5520	
Db	5580	TTCCATGGAAATTTGGGCAAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGAC	5639	
Qy	5521	AGTGTAGCACTCTACCAAGTCCAGAGCTGTGACACCTACTGTATACCCAGATGCCCCAC	5580	
Db	5640	AGTGTAGCACTCTACCAAGTCCAGAGCTGTGACACCTACTGTATACCCAGATGCCCCAC	5699	
Qy	5581	AGCCACTAC 5589		
Db	5700	AGCCACTAC 5708		

AAV62180
ID AAV62180 standard; DNA; 5711 BP

AAV62180;

DT 11-FEB-1999 (first entry)

DE BRCA1 (om1) coding sequence.

AA
KW
KW
KW
KW

BRCA1; mutation detection; disease screening; multiple allele variation;
breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;
Duchenne muscular dystrophy; Becker muscular dystrophy; ss.

Homo sapiens.

	Key	Location/Qualifiers
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PH		/*tag= a
FT		
FT		

XX
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WO9844157-A2.XX
PD 08-OCT-1998.XX
PF 26-MAR-1998: 98WC-IIS006002.

XX
PR 28-MAR-1997- 97119-00825487

XX PA (ONCO-1) ONCORMED TNC.

XX
PT
Munich PD
White MB.

XX
DP 1899-543713/46

DR P-PSDB; AAW79665.
YY

PT Identifying variations in polynucleotide sequences - using allele
PT specific hybridisation assay, sequence variation locating assay, and
PT direct sequencing in a stepwise procedure.

XX
PS Disclosure: Fig 1a-j: 62pp: English.

This sequence encodes the human BRCA (omil) protein, and was used to test the method of the invention. The method is for determining the presence or absence of a sequence variation in a gene sample, and comprises: (a) performing an allele specific hybridisation assay for one or more pre-determined sequence variations, (b) if no pre-determined sequence variation found in step (a) then performing a sequence variation location assay; (ci) if no sequence variation found in step (b) then sequencing the gene sample; (cii) if sequence variation is found in step (b) then targeted confirmatory sequencing is performed; and (d) determining the presence of a sequence variation by analysing the sequence(s) obtained in step (ci) or step (cii) against a reference sample. Alternatively, a step (a) or step (b) is omitted from the method. The invention provides a stepwise and integrated method for the efficient and accurate detection of variations in polynucleotide sequences, being directed towards screening for diseases associated with multiple allele variations, including breast and ovarian cancer, cystic fibrosis, Duchenne and Becker muscular dystrophy, and Li-Fraumeni syndrome

Sequence	5711	BP:	1953	A:	1099	C:	1277	G:	1382	T:	0	U:	0	Other:	22
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Query Match      100.0%; Score 5587.4; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 5588: Conservative 0; Mismatches 1; Indels 0;
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Db 240 CACATATTTTGCATAATTTGCATGCTGAAACTTCTCAACAGAGAGAGGCGCTTCACAG 299
QY 181 TGTCTCTTATAGTAAAGATGATATACCAAAAGAGGAGCCTACAGAAAGATGACGGAATTTAGT 240
Db 300 TGTCTCTTATAGTAAAGATGATATACCAAAAGAGGAGCCTACAGAAAGATGACGGAATTTAGT 359
QY 241 CAACCTGTGTAAGAGCTATTTGAAATCAATTTGTCTCTTTTCAGCTTTCAGCAGAGTTTGGAG 300
Db 360 CAACCTGTGTAAGAGCTATTTGAAATCAATTTGTCTCTTTTCAGCTTTCAGCAGAGTTTGGAG 419
QY 301 TATCAAAACAGCTATTAATTTTGCATAAAAGAGAAATTAATCTCTCTGACATCTTAAAGAT 360
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QY 421 GAACCCGAAATCTCTCTGAGGAAACCGTCTGAGTCCAACTCTCTCAACCTTGGGA 480
Db 540 GAACCCGAAATCTCTCTGAGGAAACCGTCTGAGTCCAACTCTCTCAACCTTGGGA 599
QY 481 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAGCTCAAAAGAGCTCTGTCTACAT 540
Db 600 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAGCTCAAAAGAGCTCTGTCTACAT 659
QY 541 GAATGGGATCTGATCTCTCTGAGGAAACCGTCTGAGTCCAACTCTCTCAACCTTGGGA 600
Db 660 GAATGGGATCTGATCTCTCTGAGGAAACCGTCTGAGTCCAACTCTCTCAACCTTGGGA 719
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QY 661 GCATAAAGGCTGCTGTGTAATTTCTGAGCGGATGAACAAATCTGAACATCATCAA 720
Db 780 GCATAAAGGCTGCTGTGTAATTTCTGAGCGGATGAACAAATCTGAACATCATCAA 839
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Db	4980	GATACTCTGGGTATAATGCAATGGAAGAAAGTGTGACGAGGGAGAAAGCCAGAAATTGACA		5039
Qy	4921	GCCTCAACAGAAAGGTCACAAAGAAATGTCATGCTGTGTGTGCTGACCCGAGAA		4980
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Qy	4981	GAATTTATGCTCGTGTACAAAGTTTGCAGAGAAAACACCACATCATCTTTAACTAATTAAT		5040
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Db	5640	AGTGTAGCACTCTACAGTGCAGGAGCTGGACACTTACCTGTGATACCCAGATGCCCCAC		5699
Qy	5581	AGCCACTTAC		5589

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC
Gapex 10.0, Gapex 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5711	100.0	5711	3 AAC60794	AAC60794 Human BRC
3	5711	100.0	5711	8 ACA61333	ACA61333 Human BRC
4	5711	100.0	5711	9 ADC63291	ADC63291 Polymorph
5	5710.6	100.0	5711	2 AAV46468	AAV46468 Human BRC
6	5710.6	100.0	5711	2 AAV46465	AAV46465 Human BRC
7	5710.6	100.0	5711	2 AAV46470	AAV46470 Human BRC
8	5710.6	100.0	5711	2 AAV46466	AAV46466 Human BRC
9	5710.6	100.0	5711	2 AAV46467	AAV46467 Human BRC
10	5710.6	100.0	5711	2 AAV46469	AAV46469 Human BRC
11	5710.6	100.0	5711	2 AAV46456	AAV46456 Human BRC
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16	5709.4	100.0	5711	3 AAC60793	AAC60793 Human BRC
17	5709.4	100.0	5711	8 ACA61332	ACA61332 Human BRC
18	5709.4	100.0	5711	9 ADC63287	ADC63287 Consensus
19	5709	100.0	5711	2 AAV46455	AAV46455 Human BRC
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26	5704.2	99.9	5711	2 AAV46459	AAV46459 Human BRC
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31	5703	99.9	5711	3 AAC60795	AAC60795 Human BRC
32	5703	99.9	5711	8 ACA61334	ACA61334 Human BRC
33	5703	99.9	5711	2 AAT17493	AAT17493 Mutated B
34	5703	99.9	5711	2 AAT17496	AAT17496 Mutated B
35	5703	99.9	5711	2 AAT17495	AAT17495 Mutated B
36	5703	99.9	5711	2 AAT17494	AAT17494 Mutated B
37	5703	99.9	5711	2 AAT17492	AAT17492 Mutated B
38	5702.6	99.9	5711	2 AAV46463	AAV46463 Human BRC
39	5702.6	99.9	5711	2 AAV46458	AAV46458 Human BRC
40	5702.6	99.9	5711	2 AAV46460	AAV46460 Human BRC
41	5701.4	99.8	5711	7 AB223502	AB223502 Nucleotid
42	5701.4	99.8	5712	2 AAT84840	AAT84840 Human bre
43	5701.4	99.8	5712	3 AA287995	AA287995 BRCAL gen
44	5701.4	99.8	5714	2 AAT18310	AAT18310 BRCAL, br
45	5701.4	99.8	5714	2 AAT17438	AAT17438 BRCAL cod

ALIGNMENTS

RESULT 1
AAV46450
ID AAV46450 standard; cDNA; 5711 BP.
XX
AC AAV46450;
XX
DT 18-NOV-1998 (first entry)
XX
DB Human BRCAL omi3 cDNA.
XX
XX BRCAL; omi3; human; breast and ovarian cancer predisposing gene;
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 120..5711
XX /*tag= a
XX /*product= "BRCAL omi3 protein"
XX
XX US5750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-00798691.
XX
XX 12-FEB-1996; 96US-00598591.
XX (ONCO-) ONCORMED INC.
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
XX Critz BS;
XX WPI; 1998-296774/26.
XX P-PSDB; AAW76100.
XX
XX BRCAL omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.
XX
XX Claim 2e; Col 55-62; 54pp; English.
XX
XX This sequence encodes the human BRCAL (breast and ovarian cancer
XX predisposing gene) omi3 gene. This sequence and polymorphic variations of
XX this sequence are useful for the identification of an individual who may

CC or may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers
XX
SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5711; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
Db |||||
Qy 1 AGCTGGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
Db |||||
Qy 61 CCTGGCTCAGGAGGCTTCACTCTCTCTCTGGTAAAGTTCAATGGAAACAGAAAGAA 120
Db CCTGGCTCAGGAGGCTTCACTCTCTCTCTGGTAAAGTTCAATGGAAACAGAAAGAA 120
Qy 121 TGGATTTATCTGCTCTGCGCTTGAAGAGTACAAATGTCATTAAGTCTATGCGAA 180
Db |||||
Qy 121 TGGATTTATCTGCTCTGCGCTTGAAGAGTACAAATGTCATTAAGTCTATGCGAA 180
Db |||||
Qy 181 TCTTAGAGTGTCCATCTCTGAGTTGATCAAGGAACTGTCTCCACAAAGTGTGACC 240
Db TCTTAGAGTGTCCATCTCTGAGTTGATCAAGGAACTGTCTCCACAAAGTGTGACC 240
Qy 241 ACATATTTTGCATTTTGCATGCTGAAGTCTCAACTCTCAACCAAGAGGCTTCAAGT 300
Db ACATATTTTGCATTTTGCATGCTGAAGTCTCAACTCTCAACCAAGAGGCTTCAAGT 300
Qy 301 GTCTTTTATGAAGATGATATAACCAAGAGGCTTCAAGATGATGATGATGATGATG 360
Db GTCTTTTATGAAGATGATATAACCAAGAGGCTTCAAGATGATGATGATGATGATG 360
Qy 361 AACTGTTTGAAGAGCTATGAAATTCATTTGCTTTTCTGAGTTGAGTGTGAGT 420
Db AACTGTTTGAAGAGCTATGAAATTCATTTGCTTTTCTGAGTTGAGTGTGAGT 420
Qy 421 ATGCAACAGCTATTAATTTTCAAAAAGGAAATTAATCTCTGCAATCTAAAGATG 480
Db ATGCAACAGCTATTAATTTTCAAAAAGGAAATTAATCTCTGCAATCTAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCCAAAAGACTTCTACAGAGT 540
Db AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCCAAAAGACTTCTACAGAGT 540
Qy 541 AACCCGAAATCCTTCTGAGGAAACCGTCTCAGTGTCCACTCTCAACCTTGGAA 600
Db AACCCGAAATCCTTCTGAGGAAACCGTCTCAGTGTCCACTCTCAACCTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGGAAAGCAGCGGATACAACTCTCAAAAGAGCTCTGTCTACATTG 660
Db CTGTGAGAACTCTGAGGAAAGCAGCGGATACAACTCTCAAAAGAGCTCTGTCTACATTG 660
Qy 661 AATTGGGATCTGATCTTCTGAAGTACCGTTTATAGGCACTTATGCGAGTGGAG 720
Db AATTGGGATCTGATCTTCTGAAGTACCGTTTATAGGCACTTATGCGAGTGGAG 720
Qy 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAAACCGGATGAAATCAGTTTGGATTCTG 780
Db ATCAAGAAATGTTTACAAATCAACCTCAAGGAAACCGGATGAAATCAGTTTGGATTCTG 780
Qy 781 CAAAAGGCTCTGTGTAATTTCTGAGCGGATGTAAGAACTGACATCATCAAC 840
Db CAAAAGGCTCTGTGTAATTTCTGAGCGGATGTAAGAACTGACATCATCAAC 840
Qy 841 CCAAGTAAATGATTTGAACCACTGAGAGAGCTGACAGGAGTCCAGAGGATCCAGAAAGT 900
Db |||||

Db 841 CCAGTAAATGATTTGAACACACCATGAGAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900
Qy 901 ATCAGGGTAGTCTTCTTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATATCTCATGCCA 960
Db |||||
Qy 901 ATCAGGGTAGTCTTCTTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATATCTCATGCCA 960
Db |||||
Qy 961 GCTCAATTACAGCATGAGAACAGCAGTCTTATTAATCTCACTAAAGACAGAAATGAATAGAAA 1020
Db GCTCAATTACAGCATGAGAACAGCAGTCTTATTAATCTCACTAAAGACAGAAATGAATAGAAA 1020
Qy 1021 AGCTGAAATCTGTATTAATAAAGCAACAGCTGGCTTACCAAGGAGCCCAACATACAGAT 1080
Db AGCTGAAATCTGTATTAATAAAGCAACAGCTGGCTTACCAAGGAGCCCAACATACAGAT 1080
Qy 1081 GGCTCGAAGTAAAGAAACATGTAAATGATAGCGGACTCCACAGCAGAAAAAAGGAGTAG 1140
Db GGCTCGAAGTAAAGAAACATGTAAATGATAGCGGACTCCACAGCAGAAAAAAGGAGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAGAAATGCGCATGCT 1200
Db ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAGAAATGCGCATGCT 1200
Qy 1201 CAGAGAAATCCTAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260
Db CAGAGAAATCCTAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAATGTTAGTCTGATGACTCACTGATG 1320
Db AAGTTAATGAGTGTGTTTCCAGAGTGAATGAATGTTAGTCTGATGACTCACTGATG 1320
Qy 1321 GGGAGTCTCAATCAAAATGCAAGTAGTGTATTTGGACGTTCTAAATAGAGTATGATG 1380
Db GGGAGTCTCAATCAAAATGCAAGTAGTGTATTTGGACGTTCTAAATAGAGTATGATG 1380
Qy 1381 AATATTCTGGTCTTCCAGAGAAATAGACTTACTGGCCAGTGTCTCATAGGCTTTAA 1440
Db AATATTCTGGTCTTCCAGAGAAATAGACTTACTGGCCAGTGTCTCATAGGCTTTAA 1440
Qy 1441 TATGTAAGTGAAGAGTCTCACTCCAAATCAGTAGAGTATATTTAGAGCAAAATAT 1500
Db TATGTAAGTGAAGAGTCTCACTCCAAATCAGTAGAGTATATTTAGAGCAAAATAT 1500
Qy 1501 TTGGGAAACCTTATCGGAAAGAGGCAAGCTCTCCCAACTTAAGCCATGTAACCTGAAATC 1560
Db TTGGGAAACCTTATCGGAAAGAGGCAAGCTCTCCCAACTTAAGCCATGTAACCTGAAATC 1560
Qy 1561 TAAATTATGAGGATTTTGTACTGAGCCACAGATATACAGAGGCTCCCTCAGAAATA 1620
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Qy 1681 CAGATTGGCAGTTCAAAAGAGCTTCTGAAATGATTAATCGGAACTTAACCAACGAGC 1740
Db CAGATTGGCAGTTCAAAAGAGCTTCTGAAATGATTAATCGGAACTTAACCAACGAGC 1740
Qy 1741 AGAATGCTCAAGTGAATATTTACTTAATAGTGTCTATGAGATTAATAAAGAGTGTAT 1800
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Qy 1801 CTAATTAGAAAGAGAAATTCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860
Db CTAATTAGAAAGAGAAATTCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860
Qy 1861 AAACGAGAGTGAACCTTATAAGCAGCAGTATAGCAATATGGAATCGCAATTAATATCC 1920
Db AAACGAGAGTGAACCTTATAAGCAGCAGTATAGCAATATGGAATCGCAATTAATATCC 1920
Qy 1921 ACAATTCAAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC 1980
Db ACAATTCAAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC 1980

QY 1981 ATGGCGTTGAACTAGTACTAGTAAATCTAAGCCACCTAAATGTGTAATGCAAA 2040
DB
QY 1982 ATGGCGTTGAACTAGTACTAGTAAATCTAAGCCACCTAAATGTGTAATGCAAA 2040
DB
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAGAAAGAGTCAACCAATGCGAGTCA 2100
DB
QY 2042 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAGAAAGAGTCAACCAATGCGAGTCA 2100
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DB
QY 2102 GGCAAGCAGAGAAACCTCAACTCATGGAAGGTAAAGAACCTGCAACTGAGCCAAAGAGA 2160
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QY 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGAATATCTTTCCAGAGCTGA 2220
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QY 2162 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGAATATCTTTCCAGAGCTGA 2220
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QY 2222 AGTTAAACAAATGCACCTGGTCTTTTACTTAAGTGTTCAAATACAGTGAATCTTAAGAAAT 2280
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QY 2282 TTGTCAATCTTAGCTTCCAGAGAGAGAAAGAGAGAACTAGAAACAGTTAAAGTGT 2340
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QY 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTTAAGTGGAGAAAGGTTTTGCCAACTG 2400
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QY 2342 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTTAAGTGGAGAAAGGTTTTGCCAACTG 2400
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DB
QY 2402 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTAATGGCACTCAGG 2460
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QY 2461 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTAATGGCACTCAGG 2520
DB
QY 2462 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTAATGGCACTCAGG 2520
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QY 2522 GTGTGAGTCAGTGTGCGACATTTGAAACCCCAAGGAGTAAATCTATGTTGTTCCAAAG 2580
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QY 2582 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCACAGTC 2640
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QY 2641 GGGAAACAGCATAGAAATGGAAGAGTGAATCTGATGCTCAGTATTTGCGAGATACAT 2700
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QY 2642 GGGAAACAGCATAGAAATGGAAGAGTGAATCTGATGCTCAGTATTTGCGAGATACAT 2700
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QY 2762 AATGTGCAACATTTCTGCGCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
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QY 3002 ACAGAACTGGACTANTACTCCAAATGAACATGAGCTTTTTCAGAAACCCATATCGTATAC 3060

QY 3061 CACCACCTTTTCCATCAAGTCAATTTGTTTAAATCTAAATGTAAAGAAATCTCTAGAGG 3120
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QY 3062 CACCACCTTTTCCATCAAGTCAATTTGTTTAAATCTAAATGTAAAGAAATCTCTAGAGG 3120
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DB
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QY 3242 CAAGCAATATTAATGAAGTGGTTCGAGTACTAATGAGTGGCTTCAGTATTAATGAAA 3300
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QY 3602 AAGATATCTAGTTTGTCTGAAATTAAGCAATTAAGGAAAGTTCTGCTGTTTTTGTAGCAAAAGCG 3660
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QY 3661 TCCAGAGAGAGAGCTTTAGCAGAGGTCCTAGCCCTTTACCCATACACATTTGGCTCAGG 3720
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QY 3841 CTACTAGGCAATAGCAGGTCCTGAGGTCCTGCTAGTAAAGTAAATATATACCTTCTCAGT 3900
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QY 3842 CTACTAGGCAATAGCAGGTCCTGAGGTCCTGCTAGTAAAGTAAATATATACCTTCTCAGT 3900
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QY 3902 TATCATTTGAAGAAATAGCTTAAATGACCTGAGTAAACCAAGTAAATTTGGCAAGGCACTC 3960
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DB
QY 3962 AGGAAACATACCTTTAGTGAGGAAACAAATGTTTCTGCTAGCTTGTCTTCTCAGTGCA 4020
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QY 4021 GTGAATTTGAAGAACTTTGACCTGCAATTAACCAACCAAGGATCTTCTTCTGATTTGTTCTT 4080
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QY 4022 GTGAATTTGAAGAACTTTGACCTGCAATTAACCAACCAAGGATCTTCTTCTGATTTGTTCTT 4080
DB
QY 4081 CCAAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGGTTGGTCTGAGTGAACAGAAATGG 4140
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QY 4082 CCAAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGGTTGGTCTGAGTGAACAGAAATGG 4140
DB
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Db 4141 TTTTCAGATGATGAGAGAGAGACCGGCTTGGAGAGAAATANTCAAGAGAGCAAGCA 4200
Qy 4201 TGGATTCAACTTAGGTGAAGCAGCATCTGGGTGAGAGAGTGAACCAAGCGTCTCTGAAG 4260
Db 4201 TGGATTCAACTTAGGTGAAGCAGCATCTGGGTGAGAGAGTGAACCAAGCGTCTCTGAAG 4260
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Qy 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCAAGATTTGACAG 5040
Db 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCAAGATTTGACAG 5040
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Db 5101 AATTATGCTGCTGATACAGTTTCCAGAAACACCAATCCTTAACTAATCTAATTA 5160
Qy 5161 CTGAAGAGACTTACTGTTTATGAAACAGAGATGCTGAGTTTGTGTGAGAGGACAC 5220
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5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGCGTAGTTAGCTATTTCTGGGTGACCC 5280
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Db 5341 TCAATGCAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGATCCCAAGGACAGAAAGATCT 5400
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Db 5401 TCAGGGGGCTAGAAATCTGTGTGCTATGGGCCCTTCCAAACATGCCCCCAGATCAACTGG 5460
Qy 5461 AATGAGATGCTACAGCTGTGTGCTTCTGTGTGAGAGGAGCTTTCATCATCCCTTG 5520
Db 5461 AATGAGATGCTACAGCTGTGTGCTTCTGTGTGAGAGGAGCTTTCATCATCCCTTG 5520
Qy 5521 GCACAGGTGTCCACCAATTTGTTGTGTGAGCAGCAATGCTTGGACAGAGCAATGGCT 5580
Db 5521 GCACAGGTGTCCACCAATTTGTTGTGTGAGCAGCAATGCTTGGACAGAGCAATGGCT 5580
Qy 5581 TCCATGCATTTGGGCGAGATGCTGTGAGCAGCTGCTGTGTGAGAGTGGTCTTGGACA 5640
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Qy 5641 GTGTAGCACTTACCACTGAGCTGAGAGCTGAGACCTACCTGATACCCCAAGATCCCCACA 5700
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Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 2
AAC60794
ID AAC60794 standard; cDNA; 5711 BP.
XX AAC60794;
AC AAC60794;
XX DT 07-FEB-2001 (first entry)
XX Human BRCA1 (om12) nucleotide sequence SEQ ID NO:3.
XX Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;
XX gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;
XX polymorphism; identification; ss.
XX Homo sapiens.
XX US6130322-A.
XX 10-OCT-2000.
XX 06-MAY-1998; 98US-00074476.
XX 12-FEB-1996; 96US-00598591.
XX 12-DEC-1997; 97US-00798691.
XX (GENE-) GENE LOGIC INC.
XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy BD;
PI Critz BS;
XX WPI; 2000-646756/62.
XX P-PSDB; AAB24218.
XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful in
XX gene therapy, especially for preventing or treating breast or ovarian
XX cancer, as well as for diagnosing or monitoring breast or ovarian cancer.
XX Claim 1; Col 45-50; 56pp; English.

XX AAC60793 to AAC60795 encode the human BRCA1 (omil-3) proteins given in
CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17
CC mapping to position 17q21. The BRCA1 (omil2) coding sequence is
CC specifically claimed in the present invention. The BRCA1 (omil2) coding
CC sequence is useful in gene therapy, especially for preventing or treating
CC breast or ovarian cancer. It is also useful for diagnosing or monitoring
CC breast or ovarian cancer. Furthermore, the BRCA1 (omil2) coding sequence
CC is useful for: (a) identifying individuals having BRCA1 gene mutations
CC and having an increased genetic susceptibility to breast or ovarian
CC cancer, or identifying a mutation that increases the genetic
CC susceptibility to breast or ovarian cancer; (b) avoiding
CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)
CC determining the presence of a previously unknown mutation in the BRCA1
CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine
CC the presence of either polymorphic alleles or mutations; and (e)
CC performing diagnosis with a reagent derived from the BRCA1 (omil) cDNA
CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,
CC which are used in an example from the present invention
XX
SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5711; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTTGGCTCAGGAGGCTTCACTCTGCTCTGGTAAAGTTCAATGGAAACAGAAAGAA 120
DB |||||
QY 121 TGGATTTATCTGCTCTGCTGTGAGAGTACAAATGTCATTAATGTCATCAGAAA 180
DB |||||
QY 181 TCTTAGAGTCTCCATCTGCTGAGTTGATCAAGAACTCTGCTCACAAGAGTGTGACC 240
DB |||||
QY 241 ACATATTTGCAATTTGCTGATGCTGAACTTCTCAACGAGAGAGGCGCTTCAAGT 300
DB |||||
QY 301 GTCTTTATCTAAGATGATATACCAAGAGGAGCTTACAGAAAGTACGAGATTTAGTC 360
DB |||||
QY 361 AACTTGTGAGAGCTATTGAAAATCAATTTGTGCTTTTCAGCTTGACACAGGTTTGGAGT 420
DB |||||
QY 421 ATGCAACAGCTATAATTTTGCAGAAAGGAGAAATTAATCTCTCTGACATCTTAAAGATG 480
DB |||||
QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGTG 540
DB |||||
QY 541 AACCGAATCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB |||||
QY 601 CTGTGAGACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB |||||
QY 661 AATTGGGATCTGATTTCTTCTGAGATACCTTTAATAGGCAACTTATAGGCAACTTATAGGCA 720
DB |||||

QY 721 ATCAAGAAATGTTTACAAATCACTCCCTCAAGGAAACCGAGGATGAAATCACTTTGGATTCTG 780
DB |||||
QY 781 CAAAGAGGCTCTGTAATTTCTGAGACCGGATGTAACAAATCTGACATCATCAAC 840
DB |||||
QY 841 CCAAGTAATTAATGTTGAACACCACTGAGAAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT 900
DB |||||
QY 901 ATCAGGAGTGTCTGTTTCAAACTGTCATGTGGGCAATGTGGCACAATATCTCATGCCA 960
DB |||||
QY 961 GCTCATTACAGCATCAGAAACAGCAGTTTAACTCACTAAACACAGAAATGAATGTAGAAA 1020
DB |||||
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DB |||||
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DB |||||
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DB |||||
QY 1201 CAGAGAACTCTAGAGTCTGAGAGTGTCTTCTGAGTAACTGATGATGATGATGATGATGATG 1260
DB |||||
QY 1261 AAGTTAAATGAGTGTCTTCCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1320
DB |||||
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1380
DB |||||
QY 1381 AATATTTCTGTTCTTCCAGAGAAATAGACTTACTGCGCAGTGTATCTCATGAGGCTTTAA 1440
DB |||||
QY 1441 TATGTAAGAGTGAAGAGTTCCTCAAAATCAGTGAAGATTAATTTGAAGACAAATAT 1500
DB |||||
QY 1501 TTGGGAAACCTTATCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
DB |||||
QY 1561 TAATATAGGAGCATTTGTTACTGAGCCACAGATTAATCAAGAGGCTGCTCCCTCACAATA 1620
DB |||||
QY 1621 AATTAAGGCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
DB |||||
QY 1681 CAGATTTGCGAGTTCAGAAAGCTCTGAAATGATAAATCAGGAGGAGGAGGAGGAGGAGGAG 1740
DB |||||
QY 1741 AGAATGGTCAAGTGAATTAATTAATAGTGTGATGATGATGATGATGATGATGATGATGATG 1800
DB |||||

1801 CTATTGAGTGAAGAAATCTTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860
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1861 AAAAGAAAGCTGAACTTAAGCAGCAGTATAGCAATATGCACTCGAAATTAATAATCC 1920
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1981 ATGCGCTTGAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 2040
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2581 ATAAATAGAAATGACACAGAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAG 2640
2581 ATAAATAGAAATGACACAGAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAG 2640
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2641 GGGAAACAGGATAGAAATGAGAGAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT 2700
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2761 AATGTGCAATCTCTGCGCACTCTGGGCTCTTAAGAAACAAAGTCCAAAAGTCACTT 2820
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2941 ATGCAAAATGCTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTGAGAGCA 3000
3001 ACAGAACTGCACTCAATTTCTCCAAATAAATCAATGCACTTTTACAAAACCCATATCGTATAC 3060
3001 ACAGAACTGCACTCAATTTCTCCAAATAAATCAATGCACTTTTACAAAACCCATATCGTATAC 3060
3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAATCTAAATCTAAATCTAAATCTAAATCT 3120
3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAATCTAAATCTAAATCTAAATCTAAATCT 3120
3121 AAAATTTGAGGAACTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAATGAGAAAT 3180
3121 AAAATTTGAGGAACTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAATGAGAAAT 3180
3181 GTACAGTACGACCAATTTAGCGGTAAATCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 3240
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Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 3
ACA61333
ID ACA61333 standard; cDNA; 5711 BP.
XX ACA61333;
AC ACA61333;
DT 07-AUG-2003 (first entry)
XX Human BRCA1 allele omi2, cDNA.
DE Human; ss; gene; BRCA1; omi2; gene therapy; tumour; breast cancer;
KW ovarian cancer; prostate cancer; colon cancer; SNP;
KW single nucleotide polymorphism.
XX Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 120..5711
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FT /product= "BRCA1 omi2"
FT replace(2201,C)
FT /*tag= b
FT /note= "single nucleotide polymorphism"
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FT replace(4956,A)
FT /*tag= h
FT allele /notes= "Single nucleotide polymorphism"
XX

US2003022184-A1.

XX 30-JAN-2003.

XX 22-OCT-2001; 2001US-00982828.

XX 12-FEB-1996; 96US-00598591.

XX 12-FEB-1997; 97US-00798691.

XX 06-MAY-1996; 98US-00074453.

XX (ONCO-) ONCORMED INC.

XX Murphy PD, Allen ACP, Alvares CP, Critz BS, Olson SJ, Thurber D;
XX Zeng B;

XX WPI; 2003-456286/43.

XX P-PSDB; ABU61604.

XX New protein sequence comprising an amino acid sequence derived from the
XX BRCA1 omi1, omi2 or omi3 sequence useful in performing gene therapy for
XX treating patients suspected of having tumor, e.g. breast, ovarian,
XX prostate or colon cancer.

XX Claim 5; Page 25-28; 60pp; English.

XX The invention relates to a protein sequence comprising an amino acid
XX sequence derived from the human BRCA1 omi1, omi2 or omi3 sequences
XX appearing as ABU61603 ABU61605. Also included are determining the
XX consensus genomic sequence or consensus coding sequence for a target
XX gene, oligonucleotide probes (each capable of hybridizing to a sample
XX BRCA1 omi gene/cDNA appearing as ACA61332-ACA61334) or their complements,
XX a chip array having n elements for performing allele specific sequence-
XX based techniques comprising a solid phase chip and oligonucleotides
XX having n different nucleotide sequences (where n is an integer greater
XX than or equal to 7, where the oligonucleotides are bound to the solid
XX phase chip in a manner that permits the oligonucleotides to effectively
XX hybridize to complementary oligonucleotides or polynucleotides, and the
XX oligonucleotides having different nucleotide sequence are bound to the
XX solid phase chip at different locations so that a particular location on
XX the solid phase chip exclusively binds oligonucleotides having a specific
XX nucleotide sequence, and the oligonucleotides are capable of specifically
XX hybridizing to the BRCA1 omi DNA), performing gene therapy on a patient,
XX treating a patient suspected of having a tumor, a expression/cloning
XX vector comprising the BRCA1 DNA sequence (or fragments), preventing the
XX formation or growth of a tumor, a host cell transformed with the vector
XX and an anti-BRCA1 antibody. The protein sequences are useful in
XX performing gene therapy for treating patients suspected of having a
XX tumor, e.g. breast cancer, ovarian cancer, prostate cancer or colon
XX cancer. The antibody is useful as an immunogen. The present sequence is a
XX cDNA representing the omi2 allele of the BRCA1 gene

SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5711; DB 8; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGTGACATCTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATACTGGGCC 60

Db QY 1 AGCTCGTGACATCTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATACTGGGCC 60

Db QY 61 CCTGCGCTCAGGAGGCGCTTCAACCTCTGCTCTGGTAAAGTTTCAATTGGAAACAGAAAGAAA 120

Db QY 61 CCTGCGCTCAGGAGGCGCTTCAACCTCTGCTCTGGTAAAGTTTCAATTGGAAACAGAAAGAAA 120

Db QY 121 TGGATTTATCTGCTCTGCGGTTGAAGAGTACAAATGTCAATTAATCTATGTCATGAGAAA 180

Db QY 121 TGGATTTATCTGCTCTGCGGTTGAAGAGTACAAATGTCAATTAATCTATGTCATGAGAAA 180

Db QY 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240

Db QY 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240

Db QY 241 ACATATTTTGGCAAAATTTTGATGCTGAAAATCTTCTCAACCCAGAGAAAGGCGCTTCACAGT 300

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Db QY 361 AACTTGTGTAAGAGTATGAAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420

Db QY 361 AACTTGTGTAAGAGTATGAAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420

Db QY 421 ATGCAAAACAGCTAATTTTGCRAAAAGGAAATTAATCTCTCTGACATCTAAAGATG 480

Db QY 421 ATGCAAAACAGCTAATTTTGCRAAAAGGAAATTAATCTCTCTGACATCTAAAGATG 480

Db QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGAGCTTCTACAGAGTG 540

Db QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGAGCTTCTACAGAGTG 540

Db QY 541 AACCCGAAATCCCTTCTGCGAGAAACAGTCTCAGTGTCCACTCTCTAAACCTCGAA 600

Db QY 541 AACCCGAAATCCCTTCTGCGAGAAACAGTCTCAGTGTCCACTCTCTAAACCTCGAA 600

Db QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAGAGACCTGTCTGTACATTG 660

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Db QY 661 AATTGGATCTGATCTCTTGAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720

Db QY 721 ATCAAGAAATGTTTCAAAATCAACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATTCTG 780

Db QY 721 ATCAAGAAATGTTTCAAAATCAACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATTCTG 780

Db QY 781 CAAAAAGGCTGTGTTGAAATTTTCTGAGACCGATGTAAACAATATCTGAACATCATCAAC 840

Db QY 781 CAAAAAGGCTGTGTTGAAATTTTCTGAGACCGATGTAAACAATATCTGAACATCATCAAC 840

Db QY 841 CCAGTAAATATGATTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCAATCCAGAAAGT 900

Db QY 841 CCAGTAAATATGATTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCAATCCAGAAAGT 900

Db QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGTGAGCCATGTGGCAAAATFACATCATGCCA 960

Db QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGTGAGCCATGTGGCAAAATFACATCATGCCA 960

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Db QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCGCTGGCTTAGCAAGGAGCAACATAACAGAT 1080

Db QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCGCTGGCTTAGCAAGGAGCAACATAACAGAT 1080

Db QY 1081 GGGCTGGAGTAAAGAAACATGTATGATAGCGGAGCTCCAGCCACAGAAAAAAGGTAG 1140

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Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGCAATAGCAGAAATCGCATGCT 1200
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DB 5701 GGCACCTACTGA 5711

RESULT 5
AAV46468
ID AAV46468 standard; cDNA; 5711 BP.
AC AAV46468;
XX 18-NOV-1998 (first entry)
DE Human BRCA1 omi3 polymorphism #4 cDNA.
KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
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FT /product= "BRCA1 omi3 protein"
FT 3232
FT variation /*tag= b
FT /*note= "This polymorphic variation can be an A or G
FT nucleotide"
XX US5750400-A.
XX 12-MAY-1998.
XX 12-FEB-1997; 97US-00798691.
XX 12-FEB-1996; 96US-00598591.
XX (ONCO-) ONCORMED INC.
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
XX Critz BS;
XX WPI; 1998-296774/26.
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to breast
XX or ovarian cancer.

PS Claim 2e; Page; 54pp; English.
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
CC nucleotide 3232. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer. The
CC sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers. NOTE: This
CC sequence does not appear in the specification but has been created from
CC the wild type BRCA1 omi3 gene represented in AAV46450
XX
SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;
Query Match 100.0%; Score 5710.6; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTCGCTGAGACTTCTCTGGACCCCGCACCCAGGCTGTGGGGTTTCTCAGATAAATGGGCC 60
DB 1 AGCTCGCTGAGACTTCTCTGGACCCCGCACCCAGGCTGTGGGGTTTCTCAGATAAATGGGCC 60
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DB 61 CTTGGGCTCAGGAGCCCTTCAACCTCTGCTCTGGTAAAGTTCAATTCGACAGAGAGAA 120
QY 121 TGGATTTATCTGCTCTTGGGTTTGAAGAAGTACAAATGTCATTAATGCTATGACAGAAA 180
DB 121 TGGATTTATCTGCTCTTGGGTTTGAAGAAGTACAAATGTCATTAATGCTATGACAGAAA 180
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DB 721 ATCAGAAATGTTACAAATCACCCCTCAAGGAAACCCAGGGATGAAATCAGTTGATTCGT 780

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Qy	901	ATCAGGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATAATACTCATGCCA	960
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Db	961	GCTCATTAACAGCATGAGACAGCAGCTTTATTACTCACTAAAGACAGATGAATGTAGAAA	1020
Qy	1021	AGGCTGAATTCGTATAAAGCAACAGCCTGGCTTAGCAGGAGCCAAATACACAGAT	1080
Db	1021	AGGCTGAATTCGTATAAAGCAACAGCCTGGCTTAGCAGGAGCCAAATACACAGAT	1080
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Db	1561	TAAATTAGGAGCAATTTGTTACTTGAGCCACAGATTAATCAGAGCGTCCCTCACAATA	1620
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Db	1621	AAATAAAGCGTAAAAGGAGACCTACATCAGCGCTTCATCTCGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTGGCAGTTCAAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAAAACGGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAAAACGGAGC	1740
Qy	1741	AGAATGCTCAAGTGAATGAAATATTACTAATAGTGTGATGAGATAAATAAAAGAGGTGATT	1800
Db	1741	AGAATGCTCAAGTGAATGAAATATTACTAATAGTGTGATGAGATAAATAAAAGAGGTGATT	1800
Qy	1801	CTATTCAAGATGAGAAAAATCCTTAACCCAAATAGAACTCACTCGAAAAAAGATCTGCTTCA	1860
Db	1801	CTATTCAAGATGAGAAAAATCCTTAACCCAAATAGAACTCACTCGAAAAAAGATCTGCTTCA	1860

Qy	1861	AAA	CGAAGCTG	AACCTT	ATAAG	CAGCAGT	ATATAG	CAATATG	CGAACTATG	CGAACTCG	GAATTA	ATATCC	1921					
Db	1861	AAA	CGAAGCTG	AACCTT	ATAAG	CAGCAGT	ATATAG	CAATATG	CGAACTATG	CGAACTCG	GAATTA	ATATCC	1921					
Qy	1921	ACA	ATTCAAAAG	CACTT	AAAAA	GAATAG	GGCTG	GAGGAGAA	GTCTTCT	TAC	CAGGCA	TATTC	1980					
Db	1921	ACA	ATTCAAAAG	CACTT	AAAAA	GAATAG	GGCTG	GAGGAGAA	GTCTTCT	TAC	CAGGCA	TATTC	1980					
Qy	1981	ATG	CGCTTG	GAAC	TAGT	AGT	CAGT	AGAAATCT	TAG	CCCACT	TAATTTG	TACTG	CAATTC	2040				
Db	1981	ATG	CGCTTG	GAAC	TAGT	AGT	CAGT	AGAAATCT	TAG	CCCACT	TAATTTG	TACTG	CAATTC	2040				
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Db	2041	TTG	TAGT	TGTTTCT	TAG	CAGT	GAAGAG	ATAAG	GAAGAA	AAAAA	AGTCA	CAACCA	ATG	CCAGT	CA	2100		
Qy	2101	GGC	ACG	CA	GAA	AACTT	CA	ACTG	AAAGG	TAA	AGAACT	CG	AACTG	GA	CCG	CA	2160	
Db	2101	GGC	ACG	CA	GAA	AACTT	CA	ACTG	AAAGG	TAA	AGAACT	CG	AACTG	GA	CCG	CA	2160	
Qy	2161	GTA	ACAAG	CCAA	ATG	AA	CAGA	CAAGT	AAAA	A	AGATGA	CTATTTCC	CAG	AGCTGA			2220	
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Qy	2221	AGT	TAA	CABA	ATG	CA	CTGGT	TCTTTT	TACT	TAAGT	GTTC	AAATF	CA	CGT	AGCTT	TA	2280	
Db	2221	AGT	TAA	CABA	ATG	CA	CTGGT	TCTTTT	TACT	TAAGT	GTTC	AAATF	CA	CGT	AGCTT	TA	2280	
Qy	2281	TTG	TCA	ATCCT	TAG	CC	TTT	CAA	GAGA	GA	AAAA	GAAG	AA	CTAG	AA	CAAGT	TTAA	2340
Db	2281	TTG	TCA	ATCCT	TAG	CC	TTT	CAA	GAGA	GA	AAAA	GAAG	AA	CTAG	AA	CAAGT	TTAA	2340
Qy	2341	CTA	TAT	ATG	CTG	TAG	AG	ACCC	CA	AA	AGATCT	CA	TGTTT	AGT	CG	GA	AA	2400
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Qy	2401	AA	AGATCT	G	TAG	AG	AGT	TAG	CA	CTG	CTG	TAT	TG	CA	CT	CA	AG	2460
Db	2401	AA	AGATCT	G	TAG	AG	AGT	TAG	CA	CTG	CTG	TAT	TG	CA	CT	CA	AG	2460
Qy	2461	AA	AGTATCT	CG	TTT	CTG	GAAGT	TAG	CA	CTG	AGG	GA	GC	AAAA	CA	GA	AC	2520
Db	2461	AA	AGTATCT	CG	TTT	CTG	GAAGT	TAG	CA	CTG	AGG	GA	GC	AAAA	CA	GA	AC	2520
Qy	2521	GTG	TG	AGT	CTAG	TG	CA	GA	AAATTTG	AAAA	CCCC	AA	GGGA	CTA	ATTCA	TG	GT	2580
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Db	2581	ATA	AT	TAGA	ATG	CA	CA	GAAG	GC	TTT	TAA	GTAT	CCAT	TTG	GG	CA	CA	2640
Qy	2641	GG	GA	ACA	AG	CA	TAG	AAAT	TGG	AA	GA	AA	AGT	CA	ATTG	AT	TG	2700
Db	2641	GG	GA	ACA	AG	CA	TAG	AAAT	TGG	AA	GA	AA	AGT	CA	ATTG	AT	TG	2700
Qy	2701	TCA	AG	GT	TTT	CA	AA	GGCC	CAGT	CA	TTT	GC	TCTG	TTT	CA	AA	T	2760
Db	2701	TCA	AG	GT	TTT	CA	AA	GGCC	CAGT	CA	TTT	GC	TCTG	TTT	CA	AA	T	2760
Qy	2761	AAT	GT	CG	AA	CA	ATTCT	CTG	CCCACT	CTG	GGT	CTCTT	AA	GA	AA	CA	AA	2820
Db	2761	AAT	GT	CG	AA	CA	ATTCT	CTG	CCCACT	CTG	GGT	CTCTT	AA	GA	AA	CA		

QY	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCAATCTCAGTTTCAGAGCA	3000
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QY	3001	ACGAACTGGGACTCAATTACTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC	3060
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QY	3061	CACCATTTTCCCAATCAAGTCATTTGTTTAAACCTAAATGTGTAAAGAAATCTCGTAGAG	3120
DB	3061	CACCATTTTCCCAATCAAGTCATTTGTTTAAACCTAAATGTGTAAAGAAATCTCGTAGAG	3120
QY	3121	AAATCTTTGAGGAACATTTCAATGTCACTCTGAAAGAGAAATGGGAAATGAGAAACATTCCTAA	3180
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QY	3181	GTACAGTGAGCACATTTAGCCGTATATAACATTTAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
DB	3181	GTACAGTGAGCACATTTAGCCGTATATAACATTTAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
QY	3241	CAAGCAATTTAATGAGTAGGTTTCCAGTACTAATGAGTGGGCTCCAGTATTAAATGAAA	3300
DB	3241	CAAGCAATTTAATGAGTAGGTTTCCAGTACTAATGAGTGGGCTCCAGTATTAAATGAAA	3300
QY	3301	TAGGTTCCAGTGTATGAAACATTTCAAGCAGAACTAGGTTAGAAAAACAGAGGCGCCAAAATTGA	3360
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QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGTCCTATAACAAAGTCCTTCCTGGAA	3420
DB	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGTCCTATAACAAAGTCCTTCCTGGAA	3420
QY	3421	GTAATTGTAAGCATCTCTGAAATATAAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTTA	3480
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QY	3481	ATACAGATTTCTTCCATATCTGATTTTCAGATAACTTTAGAACAGCCTPATGGGAAGTAGTC	3540
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QY	3601	AAGATACCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTATAGCAAAAGCG	3660
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QY	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCCCTCAGAAAGAACTTATCTTAGTGAGGATG	3780
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QY	3781	AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAAGTAAACATATACCTTTCTCAGT	3840
DB	3781	AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAAGTAAACATATACCTTTCTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGTCTACACAGTCTGCTTAGAAGACACAGAGGAGAAATTTAT	3900
DB	3841	CTACTAGGCATAGCACCGTCTACACAGTCTGCTTAGAAGACACAGAGGAGAAATTTAT	3900
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[illegible]

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5161	DB	CT	GAGAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTTGTGTGTGAACGGACAC	5220
5221	QY	TG	AAATATTTTCTAGGAATTCGGGAGGAAAATGGGTAGTTAGCTATTTCTTGGGTGACCC	5280
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5281	QY	AG	CTATTTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
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5341	QY	TC	AATGGAAGAAACCAACCAAGGTCCTAAAGCGAGAGAGAAATCCAGGACAGAAAGATCT	5400
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5401	QY	TC	AGGGGCTAGAAAATCTGTTGCTATGGGCGCTTCACCAATGCCCCACAGATCAACTGG	5460
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5461	QY	AA	TGAGTGTGTACAGCTGTGTGGTCTCTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG	5520
5461	DB	AA	TGAGTGTGTACAGCTGTGTGGTCTCTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG	5520
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5521	DB	GC	ACAGTGTGTCCACCAATTTGTGGTTGTGAGCCAGATGCTGGACAGAGGACAATGGCT	5580
5581	QY	TC	ATGCAATTTGGGACAGATGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
5581	DB	TC	ATGCAATTTGGGACAGATGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
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RESULT 6

AAV46465

ID AAV46465 standard; cDNA; 5711 BP.

XX

AC AAV46465;

DT 18-NOV-1998 (first entry)

[illegible]

DE Human BRCA1 omi3 polymorphism #1 cDNA.

KW BRCA1; om13; human; breast and ovarian cancer; susceptibility; anti-oxidant; polymorphism

KW polymorphism; susceptibility; anti-chromosome 17q; ss

XX
ММ
СЛУЖБОВИЕ Т/Д; ВЗ.

Os Homo sapiens.

33 XX
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PT variation 2201

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FT
/note="This polymer
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12-FEB-1996; 96US-00598591.
(ONCO-) ONCORMED INC.
Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
Critz BS;
WPI; 1998-2967774/26.
BRCA1 omi gene coding sequences - useful for distinguishing between
polymorphisms and mutation(s) in the screening for disposition to breast
or ovarian cancer.
Claim 2e; Page; 54pp; English.
This sequence encodes a human BRCA1 (breast and ovarian cancer
predisposing gene) omi3 gene in which a polymorphic variation occurs at
nucleotide 2201. This sequence and other polymorphic variations of this
sequence are useful for the identification of an individual who may or
may not have an increased susceptibility to breast or ovarian cancer. The
sequences used identify gene changes which are due to polymorphisms,
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
suppressor) which is involved in genetic inheritance of cancers,
especially breast and ovarian cancer. It is found at human chromosome 17q
which is known to be linked to cancer susceptibility, especially breast
cancer. Cells containing a mutation in this gene lose the wild-type
function of BRCA1 and are more susceptible to cancers. NOTE: This
sequence does not appear in the specification but has been created from
the wild type BRCA1 omi3 gene represented in AAV46450
Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;

Query Match	100.0%;	Score 5710.6;	DB 2;	Length 5711;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5710;	Conservative	1;	Mismatches	0;
Indels	0;	Gaps	0;	

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Qy	61	CTTGGCGCTCAGGAGGCGCTTCACCCCTCTGCTCTGGGTAAAGTTTCATTGGAAACAGAAAGAAA	120
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Qy	121	TGGAATTATCTGCTCTTTCGGGTGGAAGAGTACAAAATGTCATTATATGCTATGCGAGAAA	180
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Qy	301	GTCCCTTTATGTAGAATGATATAACCAAGGAGGCGCTACAAGAAAGTACAGAGATTTAGTC	360
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 Db 5701 GCCACTACTGA 5711

RESULT 8
AAV46466

ID XX AAV46466 standard; cDNA; 5711 BP.
 AC AAV46466;
 XX 18-NOV-1998 (first entry)
 DT XX Human BRCA1 omi3 polymorphism #2 cDNA.
 DE BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 KW chromosome 17q; ss.
 KW Homo sapiens.
 OS
 FH Key Location/Qualifiers
 CDS 120..5711
 FT /*tag= a
 FT /product= "BRCA1 omi3 protein"
 FT variation 2430
 FT /*tag= b
 FT /note= "This polymorphic variation can be a T or C
 nucleotide"
 FT
 XX US5750400-A.
 XX 12-MAY-1998.
 XX 12-FEB-1997; 97US-00798691.
 XX 12-FEB-1996; 96US-00598591.
 XX (ONCO-) ONCORMED INC.
 XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelker DB, Allen AC;
 XX Critz BS;
 XX WPI; 1998-296774/26.
 XX
 XX BRCA1 omi gene coding sequences - useful for distinguishing between
 XX polymorphisms and mutation(s) in the screening for disposition to breast
 XX or ovarian cancer.
 XX
 XX Claim 2e; Page; 54pp; English.
 XX This sequence encodes a human BRCA1 (breast and ovarian cancer
 XX predisposing gene) omi3 gene in which a polymorphic variation occurs at
 XX nucleotide 2430. This sequence and other polymorphic variations of this
 XX sequence are useful for the identification of an individual who may or
 XX may not have an increased susceptibility to breast or ovarian cancer. The
 XX sequences used identify gene changes which are due to polymorphisms,
 XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 XX suppressor) which is involved in genetic inheritance of cancers,
 XX especially breast and ovarian cancer. It is found at human chromosome 17q
 XX which is known to be linked to cancer susceptibility, especially breast
 XX cancer. Cells containing a mutation in this gene lose the wild-type
 XX function of BRCA1 and are more susceptible to cancers. NOTE: This
 XX sequence does not appear in the specification but has been created from
 XX the wild type BRCA1 omi3 gene represented in AAV46450
 XX
 SQ Sequence 5711 BP; 1953 A; 1097 C; 1277 G; 1383 T; 0 U; 1 Other;
 Query Match 100.0%; Score 5710.6; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGTCTGCTGAGATCTCTGAGACCCGACAGGCTGTGGGTTTCTCAGATACTGGCC 60
 Db 1 AGTCTGCTGAGATCTCTGAGACCCGACAGGCTGTGGGTTTCTCAGATACTGGCC 60
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Db 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGTATCAGAACCTGTCTCCCAAAAGTGTGACC 240
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Db 781 CAAAAAGGCTGCTTTGTGAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840
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Db 841 CCAGTAAATGATTTTGAACCACTTGAAGAGCGTGTGAGGCGATCCAGAAAGT 900
QY 901 ATCAGGCTAGTTCTGTTTCAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960
Db 901 ATCAGGCTAGTTCTGTTTCAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960
QY 961 GCTCATACAGTACAGAAACAGTATTAATCTCACTAAAGACAGATGATGAGAA 1020
Db 961 GCTCATACAGTACAGAAACAGTATTAATCTCACTAAAGACAGATGATGAGAA 1020
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTACAGAGGAGCCAAACATACAGAT 1080
Db 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTACAGAGGAGCCAAACATACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCCGATCTCCAGCAAGAAAGAGT 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCCGATCTCCAGCAAGAAAGAGT 1140
QY 1141 ATCTGAATCTGATCCCTGCTGTGAGAAAGATGGAATTAACAGAACTGCGCATGCT 1200
Db 1141 ATCTGAATCTGATCCCTGCTGTGAGAAAGATGGAATTAACAGAACTGCGCATGCT 1200
QY 1201 CAGGAATCTCAGAGATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260

Db 1201 CAGGAATCTCAGAGATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260
QY 1261 AAGTTAATGATGCTTTTCCAGAAAGTATGAACTGTAGTTCTGATGACTCATGATG 1320
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QY 1321 GGGAGTCTGAATCAAAATGCGCAAGTATGATGATTTTGGAGCTTTAAATGAGGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCGCAAGTATGATGATTTTGGAGCTTTAAATGAGGTAGATG 1380
QY 1381 AATATTTCTGCTTCTCAGAAATATAGACTTACTTGGCCAGTATCTCATGAGGCTTTAA 1440
Db 1381 AATATTTCTGCTTCTCAGAAATATAGACTTACTTGGCCAGTATCTCATGAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500
Db 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT 1500
QY 1501 TTGGGAAACCTATCGGAGAAAGGCAAGCTTCCCAACTTAAAGCCATGTAAGTAAATC 1560
Db 1501 TTGGGAAACCTATCGGAGAAAGGCAAGCTTCCCAACTTAAAGCCATGTAAGTAAATC 1560
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QY 1621 AATTAAGCGTAAAGAGACCTTACATCAGGCGTTCATCTCAGGAGTTTATCAAGAAAG 1680
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QY 1681 CAGATTTGGCAGTTTCAAAAGACTTCTGAAATGATTAATCAGGAACTTAACCAACGAGC 1740
Db 1681 CAGATTTGGCAGTTTCAAAAGACTTCTGAAATGATTAATCAGGAACTTAACCAACGAGC 1740
QY 1741 AGAATGCTCAAGTGAATTAATTAATAGTCTCATGAGATAAACAACAAAGTGAAT 1800
Db 1741 AGAATGCTCAAGTGAATTAATTAATAGTCTCATGAGATAAACAACAAAGTGAAT 1800
QY 1801 CTATTCAGATGAGAAATCTTAAACCCATAGAACTTCACTCGAAAGAGATCTGCTTCA 1860
Db 1801 CTATTCAGATGAGAAATCTTAAACCCATAGAACTTCACTCGAAAGAGATCTGCTTCA 1860
QY 1861 AAAAGGCTGAACCTTATAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATCC 1920
Db 1861 AAAAGGCTGAACCTTATAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATCC 1920
QY 1921 ACAATTCAAAGCACCTTAAAGAAATAGGCTGAGGAGAAAGTCTTACAGGCAATTC 1980
Db 1921 ACAATTCAAAGCACCTTAAAGAAATAGGCTGAGGAGAAAGTCTTACAGGCAATTC 1980
QY 1981 ATGCGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCACCTAATTTGTAATGCAAA 2040
Db 1981 ATGCGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCACCTAATTTGTAATGCAAA 2040
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCGAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCGAGTCA 2100
QY 2101 GGCACAGCAAAACCTTACAACTCATGGAAGTAAAGAACTGCAACTGAGGAGCAAGAA 2160
Db 2101 GGCACAGCAAAACCTTACAACTCATGGAAGTAAAGAACTGCAACTGAGGAGCAAGAA 2160
QY 2161 GTAAAGCCAAATGAAACAGACAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220
Db 2161 GTAAAGCCAAATGAAACAGACAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220
QY 2221 AGTTAAAGTCAATGCACTGCTTCTTACTAAGTGTCAATACAGTCAAGTCAATTAAGAT 2280
Db 2221 AGTTAAAGTCAATGCACTGCTTCTTACTAAGTGTCAATACAGTCAAGTCAATTAAGAT 2280
QY 2281 TTGTCAATCTTACGCTTCCAGAGAGAGAAAGAGAGAACTTAGAAACAGATTTAAAGTGT 2340

Db 2281 TTGTCATCTTAGCCTTCCAAAGAGAGAAAGAAAGAGAGAACTAGAAAAAGCTTAAAGTGT 2340
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Db 2341 CTAATAATGCTGAGAGACCCCAAGAGATCTCATGTTAAAGTGGAGAAAGGGTTTTGCAACTG 2400
Qy 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460
Qy 2461 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2520
Db 2461 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2520
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Db 2521 GTGTGAGTCACTGTGAGCAGTATTTGAAAAACCCCAAGAGGACTAAATTCATGGTGTTCCAAAG 2580
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Db 2581 ATATAGAAATGACACAGAGAGCTTTAAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640
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Db 2641 GGGAAAAAAGCATAGAAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
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Db 2761 AATGTGCAACATTTCTGTCCACACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
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Db 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCTCTGAC 2880
Qy 2881 AGACAGTTATATCACTGAGGCTTCTGTGGTGTGTCAGAGATGAAGCCAGTTGATA 2940
Db 2881 AGACAGTTATATCACTGAGGCTTCTGTGGTGTGTCAGAGATGAAGCCAGTTGATA 2940
Qy 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000
Db 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000
Qy 3001 ACGAACTGCACTCAATCTCCAAATGAACAATGACATTTTACAAAACCCATATGCTATAC 3060
Db 3001 ACGAACTGCACTCAATCTCCAAATGAACAATGACATTTTACAAAACCCATATGCTATAC 3060
Qy 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120
Db 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120
Qy 3121 AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAATGAGAAATTCACAA 3180
Db 3121 AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAATGAGAAATTCACAA 3180
Qy 3181 GTACAGTGAGCAACAATTAGCCGTAATAATTAAGAGAAATGTTTTTAAAGGAGCCAGCT 3240
Db 3181 GTACAGTGAGCAACAATTAGCCGTAATAATTAAGAGAAATGTTTTTAAAGGAGCCAGCT 3240
Qy 3241 CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAG 3300
Db 3241 CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAG 3300
Qy 3301 TAGGTTCCAGTGATGAAGAAATTCACAGCAAACTAGGTAGAAACAGAGGCCCAAAATTTGA 3360
Db 3301 TAGGTTCCAGTGATGAAGAAATTCACAGCAAACTAGGTAGAAACAGAGGCCCAAAATTTGA 3360
Qy 3361 ATGCTATGCTTAGATAGGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTTCTCTGGAA 3420
Db 3361 ATGCTATGCTTAGATAGGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTTCTCTGGAA 3420

Qy 3421 GTAAATTTGAGCATCTGAAATTAABAAAGCAAGATATGAGAGAGTAGTTTCAAGCTCTTA 3480
Db 3421 GTAAATTTGAGCATCTGAAATTAABAAAGCAAGATATGAGAGAGTAGTTTCAAGCTCTTA 3480
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAATTAACCTTAGAACAGCCCTATCGGAAGTAGTC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAATTAACCTTAGAACAGCCCTATCGGAAGTAGTC 3540
Qy 3541 ATGCATCTCAGGTTTCTGAGACACCTGATGACCTGTTAGATGATGTTGGAATAAAGG 3600
Db 3541 ATGCATCTCAGGTTTCTGAGACACCTGATGACCTGTTAGATGATGTTGGAATAAAGG 3600
Qy 3601 AAGATACTAGTTTGTGCTGAAATGACATTAAGCAAAAGTCTGCTGTTTTTAGCAAAAGCG 3660
Db 3601 AAGATACTAGTTTGTGCTGAAATGACATTAAGCAAAAGTCTGCTGTTTTTAGCAAAAGCG 3660
Qy 3661 TCCAGAGAGAGAGCTTTAGCAGGAGCTTAGGCCCTTACCCCATACACATTTGGCTCAGG 3720
Db 3661 TCCAGAGAGAGAGCTTTAGCAGGAGCTTAGGCCCTTACCCCATACACATTTGGCTCAGG 3720
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780
Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Qy 3841 CTACTAGGATACACCGTTGCTACGAGTGTCTGTCTAGAGACACAGAGGAGAAATTTAT 3900
Db 3841 CTACTAGGATACACCGTTGCTACGAGTGTCTGTCTAGAGACACAGAGGAGAAATTTAT 3900
Qy 3901 TATCATTTGAAGAAATAGCTTTAAATGACTGCAAGTAAACAGAGTAAATTTGGCAAGGCACTCTC 3960
Db 3901 TATCATTTGAAGAAATAGCTTTAAATGACTGCAAGTAAACAGAGTAAATTTGGCAAGGCACTCTC 3960
Qy 3961 AGGAAATCACTTAGTGTAGGAGAAAGAAATGTTCTGTAGCTGTTGTTTCTTCAAGTGA 4020
Db 3961 AGGAAATCACTTAGTGTAGGAGAAAGAAATGTTCTGTAGCTGTTGTTTCTTCAAGTGA 4020
Qy 4021 GTGAATTTGAAGAACTTGAATGCAAAATACAAACACCCAGGATCTTTCTTGAATGGTCTT 4080
Db 4021 GTGAATTTGAAGAACTTGAATGCAAAATACAAACACCCAGGATCTTTCTTGAATGGTCTT 4080
Qy 4081 CCAAAATATGAGGCACTAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAAGAGAAATGG 4140
Db 4081 CCAAAATATGAGGCACTAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAAGAGAAATGG 4140
Qy 4141 TTTCAATGATGATGAAGAAAGAGGAAAGGCTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4200
Db 4141 TTTCAATGATGATGAAGAAAGAGGAAAGGCTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4200
Qy 4201 TGAATTTCAAATTTAGGTGAAGCAGATCTGGGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGA 4260
Db 4201 TGAATTTCAAATTTAGGTGAAGCAGATCTGGGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGA 4260
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTTAACTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTTAACTCAGCAGAGGATACCATGC 4320
Qy 4321 AACATAACCTGATAAAGCTTCCAGCAGGAAATGGCTGAACTAGAACTGTGTTAGAACAGC 4380
Db 4321 AACATAACCTGATAAAGCTTCCAGCAGGAAATGGCTGAACTAGAACTGTGTTAGAACAGC 4380
Qy 4381 ATGGGAGCCAGCTTCTTAACTGAGTACCTTCCATCATAGTGAATGCTTCTGCTCCTGAGG 4440
Db 4381 ATGGGAGCCAGCTTCTTAACTGAGTACCTTCCATCATAGTGAATGCTTCTGCTCCTGAGG 4440
Qy 4441 ACCTGCGAAATCCAGAAACAAAGCAATCAGAAAAAGCAGTATTAATCTTCAACAAAAAGTA 4500
Db 4441 ACCTGCGAAATCCAGAAACAAAGCAATCAGAAAAAGCAGTATTAATCTTCAACAAAAAGTA 4500

SQ		Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;									
Query Match		100.0%; Score 5710.6; DB 2; Length 5711;									
Best Local Similarity		100.0%; Pred. No. 0;									
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;											
Qy	1	AGCTGCGCTGAGACTCTCTGACCCCGCCACCGAGGCTGTGGGGTTCTTCAGATTAACCTGGGCC	60								
Db	1	AGCTGCGCTGAGACTCTCTGACCCCGCCACCGAGGCTGTGGGGTTCTTCAGATTAACCTGGGCC	60								
Qy	61	CCTGCGCTCAGAGGCGCTTCAACCCCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA	120								
Db	61	CCTGCGCTCAGAGGCGCTTCAACCCCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA	120								
Qy	121	TGGAATTAATCTGCTCTTCGCGTTGAGAGAGTACAAAATGTCAATTAATCTGATGACAGAAA	180								
Db	121	TGGAATTAATCTGCTCTTCGCGTTGAGAGAGTACAAAATGTCAATTAATCTGATGACAGAAA	180								
Qy	181	TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	240								
Db	181	TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	240								
Qy	241	ACATATTTTGCATTTTGGATGCTGAAAATCTTCTCAACCAAGAGGCGCTTTCACAGT	300								
Db	241	ACATATTTTGCATTTTGGATGCTGAAAATCTTCTCAACCAAGAGGCGCTTTCACAGT	300								
Qy	301	GTCCCTTTATGTAAGATGATATACCAAAAGGCGCTACAGAAAGTACGAGATTTAGTC	360								
Db	301	GTCCCTTTATGTAAGATGATATACCAAAAGGCGCTACAGAAAGTACGAGATTTAGTC	360								
Qy	361	AACCTGTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTGGACAGGTTTGGAGT	420								
Db	361	AACCTGTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTGGACAGGTTTGGAGT	420								
Qy	421	ATGCACACAGCTATTAATTTTGCAAAAGGAGAAATTAATCTCTTCAACATCTAAAGATG	480								
Db	421	ATGCACACAGCTATTAATTTTGCAAAAGGAGAAATTAATCTCTTCAACATCTAAAGATG	480								
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG	540								
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG	540								
Qy	541	AACCCGAAAATCTTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTTAACTTGGAA	600								
Db	541	AACCCGAAAATCTTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTTAACTTGGAA	600								
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTTCAAGAGCTGTCTACATTTG	660								
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTTCAAGAGCTGTCTACATTTG	660								
Qy	661	AATTGGGATCTGATTTCTGAGATACCGTTAATAAGGCAACTTATTGCGAGTGTGGAG	720								
Db	661	AATTGGGATCTGATTTCTGAGATACCGTTAATAAGGCAACTTATTGCGAGTGTGGAG	720								
Qy	721	ATCAAGATTTGTAACAAATCAACCTCAGGAAACAGGATGAATCAGTTTGGATTTCTG	780								
Db	721	ATCAAGATTTGTAACAAATCAACCTCAGGAAACAGGATGAATCAGTTTGGATTTCTG	780								
Qy	781	CAAAAAGGCGCTTGTGAAATTTCTGAGACGGATGTAAACAAATCTGAACTCATCAAC	840								
Db	781	CAAAAAGGCGCTTGTGAAATTTCTGAGACGGATGTAAACAAATCTGAACTCATCAAC	840								
Qy	841	CCAGTAATATGATTTGAACACCACTGAGAAAGCGTGACGCTGAGAGGATCCAGAAAAGT	900								
Db	841	CCAGTAATATGATTTGAACACCACTGAGAAAGCGTGACGCTGAGAGGATCCAGAAAAGT	900								
Qy	901	ATCAGGGTGTGTTCTGTTTCAAACTTGATGTGGAGCCATGTGGCACAATACTCATGCCA	960								
Db	901	ATCAGGGTGTGTTCTGTTTCAAACTTGATGTGGAGCCATGTGGCACAATACTCATGCCA	960								
Qy	961	GCTCATTTACAGCATGAGAAACGAGTATTTACTCACTAAAGACAGATGAATGTAGAAA	1020								
Db	961	GCTCATTTACAGCATGAGAAACGAGTATTTACTCACTAAAGACAGATGAATGTAGAAA	1020								

Qy	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTTAGCAAGAGCCAAATAACAGAT	1080								
Db	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTTAGCAAGAGCCAAATAACAGAT	1080								
Qy	1081	GGGCTGGAAGTACAGAAACATGTAATCATAGGGGGGACTCCCGCACAGAAAAAAGGTAG	1140								
Db	1081	GGGCTGGAAGTACAGAAACATGTAATCATAGGGGGGACTCCCGCACAGAAAAAAGGTAG	1140								
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAGATGAAATAAGCAGAAAATGCCATGCT	1200								
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAGATGAAATAAGCAGAAAATGCCATGCT	1200								
Qy	1201	CAGAGAAATCTAGAGATACGAAAGATGTTCTCTTGGATTAACATAATAGCAGCAATTCAGA	1260								
Db	1201	CAGAGAAATCTAGAGATACGAAAGATGTTCTCTTGGATTAACATAATAGCAGCAATTCAGA	1260								
Qy	1261	AAGTTAATGAGTGGTTTTCAGAAAGTATGAACTGTTAGGTTCTGTGATGACTCACATGATG	1320								
Db	1261	AAGTTAATGAGTGGTTTTCAGAAAGTATGAACTGTTAGGTTCTGTGATGACTCACATGATG	1320								
Qy	1321	GGGAGTCTGAATCAAAATGCAAAAGTACTGATGTTTGGACGTTCTAAATGAGGTAGATG	1380								
Db	1321	GGGAGTCTGAATCAAAATGCAAAAGTACTGATGTTTGGACGTTCTAAATGAGGTAGATG	1380								
Qy	1381	AATATTCTGCTCTCTCAGAGAAATAGACTTACTGCGCCAGTGATCTCATGAGGCTTTAA	1440								
Db	1381	AATATTCTGCTCTCTCAGAGAAATAGACTTACTGCGCCAGTGATCTCATGAGGCTTTAA	1440								
Qy	1441	TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATATTGGAAGACAAAATAT	1500								
Db	1441	TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATATTGGAAGACAAAATAT	1500								
Qy	1501	TTGGGAAACCTATCCGAGAGGAGCGCTCCCAACTTAAGCCATGTAACCTGAAATC	1560								
Db	1501	TTGGGAAACCTATCCGAGAGGAGCGCTCCCAACTTAAGCCATGTAACCTGAAATC	1560								
Qy	1561	TAATATTAGAGAGCAATTTGTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAAATA	1620								
Db	1561	TAATATTAGAGAGCAATTTGTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAAATA	1620								
Qy	1621	AATTAAAGCGTAAAGAGACCTACATCAGGCCCTTCTCTGAGGATTTTATCAAGAAAG	1680								
Db	1621	AATTAAAGCGTAAAGAGACCTACATCAGGCCCTTCTCTGAGGATTTTATCAAGAAAG	1680								
Qy	1681	CAGATTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACTAAACCAACCGAGC	1740								
Db	1681	CAGATTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACTAAACCAACCGAGC	1740								
Qy	1741	AGAATGCTCAAGTGAATATTTACTTAATAGTGGTCAATGAGAAATAAAAGGTTGAT	1800								
Db	1741	AGAATGCTCAAGTGAATATTTACTTAATAGTGGTCAATGAGAAATAAAAGGTTGAT	1800								
Qy	1801	CTATTCCAGATGAGAAATCTTAACCCATGAATCCTCGAAAGAGATCTGCTTTCA	1860								
Db	1801	CTATTCCAGATGAGAAATCTTAACCCATGAATCCTCGAAAGAGATCTGCTTTCA	1860								
Qy	1861	AAAACGAAAGCTGAACCTTAAAGCAGGATATAAGCAATATGGAACCTGAAATTAATATCC	1920								
Db	1861	AAAACGAAAGCTGAACCTTAAAGCAGGATATAAGCAATATGGAACCTGAAATTAATATCC	1920								
Qy	1921	ACAATTTCAAAGCACCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC	1980								
Db	1921	ACAATTTCAAAGCACCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC	1980								
Qy	1981	ATCGGCTTGAATAGTAGTACAGTAAATCTAAGCCACCTTAATTTGCTGAAATTCGAAA	2040								
Db	1981	ATCGGCTTGAATAGTAGTAAATCTAAGCCACCTTAATTTGCTGAAATTCGAAA	2040								
Qy	2041	TTGATAGTGTCTTACGAGTGAAGAGATAAAGAAAAGAGTACACCAANTGCCAGTCA	2100								
Db	2041	TTGATAGTGTCTTACGAGTGAAGAGATAAAGAAAAGAGTACACCAANTGCCAGTCA	2100								

QY 2101 GGCACAGCAGAAACCTCAACCTCTGGAAGGTAAAGAACCTGCAACTGAGGCCCAAGAGA 2160
DB 2101 GGCACAGCAGAAACCTCAACCTCTGGAAGGTAAAGAACCTGCAACTGAGGCCCAAGAGA 2160
QY 2161 GTAAACAAGCCAAAATGAACAGACAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA 2220
DB 2161 GTAAACAAGCCAAAATGAACAGACAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA 2220
QY 2221 AGTTAAACAAGTGAACCTGCTGTTCTTTTACTTAAGTGTTCAAATACCAAGTGAACCTTAAAGAAT 2280
DB 2221 AGTTAAACAAGTGAACCTGCTGTTCTTTTACTTAAGTGTTCAAATACCAAGTGAACCTTAAAGAAT 2280
QY 2281 TTGTCAATCTCTAGCCTTCCAGAGAGAAAGAAAGAGAAAATAGAAACAGTCTAAAGTGT 2340
DB 2281 TTGTCAATCTCTAGCCTTCCAGAGAGAAAGAAAGAGAAAATAGAAACAGTCTAAAGTGT 2340
QY 2341 CTAAATATCTGGAAGCCCAAGATCTCAATGTTAAAGTGAAGAGAGGTTTTCAGAACTG 2400
DB 2341 CTAAATATCTGGAAGCCCAAGATCTCAATGTTAAAGTGAAGAGAGGTTTTCAGAACTG 2400
QY 2401 AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGTGTAATGAGCACTCAGG 2460
DB 2401 AAAGATCTGTAGAGTAGCAGTATTTTCACTGGTACCTGTGTAATGAGCACTCAGG 2460
QY 2461 AAAGTATCTCTGTTACTGGAAGTACCTCTAGGAGGCAAAAACAGAACCAATTAAT 2520
DB 2461 AAAGTATCTCTGTTACTGGAAGTACCTCTAGGAGGCAAAAACAGAACCAATTAAT 2520
QY 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAACCCCAAGGAGCAATTAATCATGTTTCCAAAG 2580
DB 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAACCCCAAGGAGCAATTAATCATGTTTCCAAAG 2580
QY 2581 ATATATGAAATGACACAGAGGCTTTAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640
DB 2581 ATATATGAAATGACACAGAGGCTTTAAGTATCAATTTGGGACATGAAGTTAAACACAGTC 2640
QY 2641 GGGAAAACAAGCATAGAAATGGAAGAACTGAATGATCTCAGTATTTGAGCAATACAT 2700
DB 2641 GGGAAAACAAGCATAGAAATGGAAGAACTGAATGATCTCAGTATTTGAGCAATACAT 2700
QY 2701 TCAAGGTTTCAAGCGCAGCTCATTTGCTCTGTTTCAATCCAGGAAATGAGAGG 2760
DB 2701 TCAAGGTTTCAAGCGCAGCTCATTTGCTCTGTTTCAATCCAGGAAATGAGAGG 2760
QY 2761 AATGTGCAACATTTCTGCCCCACTCTGGTCTCTTAAAGAACCAAGTCCAAAGTCACTT 2820
DB 2761 AATGTGCAACATTTCTGCCCCACTCTGGTCTCTTAAAGAACCAAGTCCAAAGTCACTT 2820
QY 2821 TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCTGTAC 2880
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QY 3001 ACAGAACTGAGTCAATCTCAATTAACATGAGCTTTTACAAACCCATATGCTATAC 3060
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QY 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTAAGAAAATCTGCTAGAGG 3120
DB 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTAAGAAAATCTGCTAGAGG 3120
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DB 3121 AAAACTTTGAGGAAACATCTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCCAA 3180
QY 3181 GTACAGTGAGCACAATTAGCCGTAAATTAACATTAGAGAAAATGTTTAAAGAGGCCAGCT 3240

DB 3181 GTACAGTGAGCACAATTAGCCGTAAATTAACATTAGAGAAAATGTTTAAAGAGGCCAGCT 3240
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DB 3241 CAAGCAATATTAATGAAAGTAGGTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAAA 3300
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DB 3301 TAGCTTCCAGTGATGAAAACATTCACAGCAGAACTAGGTAGAAACAGAGGGCCAAAAATTGA 3360
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DB 3421 GTAATTTGAAGCATCTGAAAATAAAAAAGCAAGATATGAAGAGTAGTTTCAGACTGTTA 3480
QY 3481 ATACAGATTTCTTCCATATCTGATTTAGATTAACATTAAGAACAGCTATGGGAAGTAGTC 3540
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DB 3541 ATGCATCTCAGGTTTCTCTGACACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600
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DB 3601 AAGATCTAGTTTGTCTGAAAATGACATTAAGGAAAAGTTCTGCTGTTTTAGCAAAAGCG 3660
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DB 3661 TCCAGAGAGGAGCTTACAGAGGCTTAGCCCTTCCACCATACACATTTGGCTCAGG 3720
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DB 3721 GTTACCCGAGAGGGGCAAGAAATTAAGAGTCTCTCAGAGAGAACTTATCTAGTGAGATG 3780
QY 3781 AAGAGCTTCTCTGCTTCCAACTTTGTTTATTTGTTAAAGTAAACATATACCTTCTCAGT 3840
DB 3781 AAGAGCTTCTCTGCTTCCAACTTTGTTTATTTGTTAAAGTAAACATATACCTTCTCAGT 3840
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DB 3901 TATCATTTGAAGAAATAGCTTAAATGATGCTGAGTAAACAGGTAAATTTGGGCAAGGCATCTC 3960
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DB 4081 CCNAAACAAATGAGGATCTGTAAGCCAGGAGTGGTCTGAGTGCAAGGAATTCG 4140
QY 4141 TTTTCAGATGATCAAGAAAGAGGAAACCGGCTTGGAGAAAATATCAAGAGAGCAAGCA 4200
DB 4141 TTTTCAGATGATCAAGAAAGAGGAAACCGGCTTGGAGAAAATATCAAGAGAGCAAGCA 4200
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Db 4261 ACTGCTAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320
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Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAGC 4380
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Db 4501 GTGAATACCTTAAAGCCAGATCCAGAGGCTTCTCTGTCGACAGCTTTGAGGTCTCG 4560
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Qy 4621 GCCCATCATTTAGATGATAGTGGTACATGACAGTGTCTCTGGAGTCTTCAAGATAGAA 4680
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Qy 4921 AAGTTCCTCCATTTGAGATGTCAGAACTCTGCGCAGGCTCAGCTGCTGCTCATCTACTG 4980
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Db 5101 AATTATGCTGCTGTACAGTTTCCAGAAAAACACACATCACTTTAACTTAATTA 5160
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Qy 5341 TCAATGGAAGAACCCACCAAGGTTCCAAAGGAGCAAGAGATCCAGGACAGAAAGTCT 5400
Db 5341 TCAATGGAAGAACCCACCAAGGTTCCAAAGGAGCAAGAGATCCAGGACAGAAAGTCT 5400

Qy 5401 TCAGGGGGCTAGAAATCTGTGTATGGGCCCTTCCAAACATGCCCAACAGATCAACTGG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTGTATGGGCCCTTCCAAACATGCCCAACAGATCAACTGG 5460
Qy 5461 AATGGATGGTACAGCTGTGTGGTCTTCTGTGTGAAGGAGCTTTTCAATTCACCCCTTG 5520
Db 5461 AATGGATGGTACAGCTGTGTGGTCTTCTGTGTGAAGGAGCTTTTCAATTCACCCCTTG 5520
Qy 5521 GCACAGGTGTCACCCAAATTTGTGTGAGCCAGCCAGATGCTTGGACAGAGCAATGGCT 5580
Db 5521 GCACAGGTGTCACCCAAATTTGTGTGAGCCAGATGCTTGGACAGAGCAATGGCT 5580
Qy 5581 TCCATGCAATTGGGCGAGATGTGTGAGGCACTCTGTGTGAGCCAGAGTGGTGTGGACA 5640
Db 5581 TCCATGCAATTGGGCGAGATGTGTGAGGCACTCTGTGTGAGCCAGAGTGGTGTGGACA 5640
Qy 5641 GTGTAGCACTCTACCAAGTGCAGAGCTGAGACCTTACTGTATACCCAGATCCCCACA 5700
Db 5641 GTGTAGCACTCTACCAAGTGCAGAGCTGAGACCTTACTGTATACCCAGATCCCCACA 5700
Qy 5701 GCCCACTACTGA 5711
Db 5701 GCCCACTACTGA 5711

RESULT 10

AAV46469

ID AAV46469 standard; cDNA; 5711 BP.

XX AAV46469;

AC AC

XX DT

18-NOV-1998 (first entry)

XX DT

Human BRCA1 omi3 polymorphism #5 cDNA.

XX DB

XX KW

BRCA1; omi2; human; breast and ovarian cancer predisposing gene;

polymorphism; susceptibility; anti-oncogene; tumour suppressor;

chromosome 17q; ss.

XX KW

XX OS

Homo sapiens.

XX PH

Key

Location/Qualifiers

120..5711

/*tag= a

/product= "BRCA1 omi3 protein"

variation 3667

/tag= b

/note= "This polymorphic variation can be an A or G nucleotide"

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US5750400-A.

XX XX

12-MAY-1998.

XX XX

12-FEB-1997; 97US-00798691.

XX XX

12-FEB-1996; 96US-00598591.

XX XX

(ONCO-) ONCORMED INC.

XX XX

Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;

Critz BS,

XX XX

WPI; 1998-296774/36.

XX XX

BRCA1 omi gene coding sequences - useful for distinguishing between

polymorphisms and mutation(s) in the screening for disposition to breast

or ovarian cancer.

XX XX

Claim 2e; Page; 54pp; English.

XX PS

This sequence encodes a human BRCA1 (breast and ovarian cancer

CC

CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
CC nucleotide 3657. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer. The
CC sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers. NOTE: This
CC sequence does not appear in the specification but has been created from
CC the wild type BRCA1 omi3 gene represented in AAV46450
XX
SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;

Query Match 100.0%; Score 5710.6; DB 2; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGCTGCTGAGACTTCCTGGACCCCGACCGGCTGGGGTCTCAGATAAATCTGGGCC	60
Db	1	AGCTGCTGAGACTTCCTGGACCCCGACCGGCTGGGGTCTCAGATAAATCTGGGCC	60
Qy	61	CCTGGGCTCAGAGGCTTCACCCCTCTGCTCTGGGTAAAGTTTCATTGGAAACAGAAAGAA	120
Db	61	CCTGGGCTCAGAGGCTTCACCCCTCTGCTCTGGGTAAAGTTTCATTGGAAACAGAAAGAA	120
Qy	121	TGGATTTATCTGCTCTGGGTTGAAGAGTACAAATGTCATTAATCTATGAGAA	180
Db	121	TGGATTTATCTGCTCTGGGTTGAAGAGTACAAATGTCATTAATCTATGAGAA	180
Qy	181	TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC	240
Db	181	TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC	240
Qy	241	ACATATTTTGCAATTTTGATGCTGAAACTTCTCAACAGAGAAAGGGGCTTCACAGT	300
Db	241	ACATATTTTGCAATTTTGATGCTGAAACTTCTCAACAGAGAAAGGGGCTTCACAGT	300
Qy	301	GTCTTTTATGAGAGTATTAATTAACAAAGAGGCTACAGAAAGTACGAGATTAGTC	360
Db	301	GTCTTTTATGAGAGTATTAATTAACAAAGAGGCTACAGAAAGTACGAGATTAGTC	360
Qy	361	AATTTGTTGAGAGCTATGAAAAATCATTTGCTGCTTTTTCAGCTTGACACAGTTTGGAGT	420
Db	361	AATTTGTTGAGAGCTATGAAAAATCATTTGCTGCTTTTTCAGCTTGACACAGTTTGGAGT	420
Qy	421	ATGCAACAGCTATTAATTTGCAAAAAGGAAATTAATCTCTCTGAAACATCTAAAGATG	480
Db	421	ATGCAACAGCTATTAATTTGCAAAAAGGAAATTAATCTCTCTGAAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCTCAAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Db	481	AAGTTTCTATCTCAAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Qy	541	RACCCGAATCTCTCTGAGGAAACCGTCTCAGTGTCCACTCTACCTTGGA	600
Db	541	RACCCGAATCTCTCTGAGGAAACCGTCTCAGTGTCCACTCTACCTTGGA	600
Qy	601	CTGTGAGAACTCTGAGGAAACCGGATACAACTCAAAAGAGCTCTCTACATTTG	660
Db	601	CTGTGAGAACTCTGAGGAAACCGGATACAACTCAAAAGAGCTCTCTACATTTG	660
Qy	661	AATGGGATCTGATTTCTGAGGAAACCGTATTAAGGAACTTATTCGAGTGGAG	720
Db	661	AATGGGATCTGATTTCTGAGGAAACCGTATTAAGGAACTTATTCGAGTGGAG	720
Qy	721	ATCAAGAAATTTTACAAATCAACCTCAAGGAAACCGAGGATCAATCAGTTTGGATCTG	780
Db	721	ATCAAGAAATTTTACAAATCAACCTCAAGGAAACCGAGGATCAATCAGTTTGGATCTG	780
Qy	781	CAAAAAGGCTGCTTGGAAATTTTCTGAGACGGATGTAACTAACTGAAATCAATCAAC	840

Db	781	CAAAAAGGCTGCTTGGAAATTTTCTGAGACGGATGTAACTAACTGAAATCATCAAC	840
Qy	841	CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGCTGAGAGCGATCCAGAAAGT	900
Db	841	CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGCTGAGAGCGATCCAGAAAGT	900
Qy	901	ATCAGGCTAGTTCCTGTTTCAAACTTGCATCTGAGCGCATGTGGCAAAATCTCATGCCA	960
Db	901	ATCAGGCTAGTTCCTGTTTCAAACTTGCATCTGAGCGCATGTGGCAAAATCTCATGCCA	960
Qy	961	GCTCATTACAGCATGAGAACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAA	1020
Db	961	GCTCATTACAGCATGAGAACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAA	1020
Qy	1021	AGGCTGATTTCTCTTAATTAAGCAACCGCTGGCTTAGCAAGAGGCCAATACAGAT	1080
Db	1021	AGGCTGATTTCTCTTAATTAAGCAACCGCTGGCTTAGCAAGAGGCCAATACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGGGACTCCCGACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGGGACTCCCGACAGAAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAAAGAAAGTGGATTAAGCAGAACTGCCATCT	1200
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAAAGAAAGTGGATTAAGCAGAACTGCCATCT	1200
Qy	1201	CAGAGATCTCTAGAGTACTGAAAGATGTTCTCTTGGATTAACACTAAATAGCAGATTG	1260
Db	1201	CAGAGATCTCTAGAGTACTGAAAGATGTTCTCTTGGATTAACACTAAATAGCAGATTG	1260
Qy	1261	AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTTAGTTCTGATCTGATCAGATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTCCAGAAAGTGAATGTTAGTTCTGATCTGATCAGATGATG	1320
Qy	1321	GGGAGTCTGATCAAAATGCCAAAGTGTGATGTTTGGAGCTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGATCAAAATGCCAAAGTGTGATGTTTGGAGCTTCTAAATGAGGTAGATG	1380
Qy	1381	AATAFTCTGCTTCTCAGAGAAATAGACTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Db	1381	AATAFTCTGCTTCTCAGAGAAATAGACTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT	1500
Qy	1501	TTGGAAAACTTATCGGAGAGGCGAGCTCCCGCACTTAAAGCCATGTAACTGAAATC	1560
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Qy	1561	TAAATATAGAGCATTTTGTATCTGAGCCACAGATTAATACAGAGCGTCCCTCACAATA	1620
Db	1561	TAAATATAGAGCATTTTGTATCTGAGCCACAGATTAATACAGAGCGTCCCTCACAATA	1620
Qy	1621	AATTAAGCTTAAAGAGGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAA	1680
Db	1621	AATTAAGCTTAAAGAGGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAA	1680
Qy	1681	CAGATTGGCAGTTCAAAAGACTCTCGAAATGATAATCAAGGAACTTAACCAACCGGAG	1740
Db	1681	CAGATTGGCAGTTCAAAAGACTCTCGAAATGATAATCAAGGAACTTAACCAACCGGAG	1740
Qy	1741	AGATGCTCAAGTGTGAATTTACTTAATAGTGTCTCATGAGATTAACCAACAAAGGTTAT	1800
Db	1741	AGATGCTCAAGTGTGAATTTACTTAATAGTGTCTCATGAGATTAACCAACAAAGGTTAT	1800
Qy	1801	CTATTTCAGATGAGAAAAATCTTAACCAATAGATTCATCTCGMAAAGAAATCTGCTTCA	1860
Db	1801	CTATTTCAGATGAGAAAAATCTTAACCAATAGATTCATCTCGMAAAGAAATCTGCTTCA	1860
Qy	1861	AAACGAAGCTGACCTTATTAAGCAGGATATAGCAATATGGAATCGAATTAATATCC	1920

(ONCO-) ONCORMED INC.

Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC; Critz BS;

WPI; 1998-296774/26.

BRCA1 omi gene coding sequences - useful for distinguishing between polymorphisms and mutation(s) in the screening for disposition to breast or ovarian cancer.

Claim 2e; Page; 54pp; English.

This sequence encodes a human BRCA1 (breast and ovarian cancer predisposing gene) omil gene in which a polymorphic variation occurs at nucleotide 4427. This sequence and other polymorphic variations of this sequence are useful for the identification of an individual who may or may not have an increased susceptibility to breast or ovarian cancer. The sequences used identify gene changes which are due to polymorphisms, rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour suppressor) which is involved in genetic inheritance of cancers, especially breast and ovarian cancer. It is found at human chromosome 17q which is known to be linked to cancer susceptibility, especially breast cancer. Cells containing a mutation in this gene lose the wild-type function of BRCA1 and are more susceptible to cancers. NOTE: This sequence does not appear in the specification but has been created from the wild type BRCA1 omil gene represented in AAV46448

Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;

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Query Match      100.0%; Score 5710.6; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AGCTCGCTGAGACTTCTCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60

db
1 AGCTCGCTGAGACTTCCTGGA CCCCGCACCGCTGTGGGTTT CTCAGATAACTGGGC 60

QY 61 CCTGCGCTCAGGAGGCCCTTCACCCCTCTGCTCTGGGTAAGTTCA TTGGAACAGAAAGAAA 120

[illegible]

121 TGGATTATCTGCTCTTCGCCGTGAAGAAGTACAAAATGTCATTATGCTATGCAGAAA 180

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

[illegible][illegible]

Ques	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Ques	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

QY
241 ALATATTTTGCATAATTTTGCATGCTGAACTTCTCAATCAGAGAAAGGGCTTTCACAGT 300

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505 5TCCCTTATGTAGGATGATATATATACCAATTAAGGAGGCTTACAGAGAAAGTACGAGATTAGTC 360

361 AACCTTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTCAGCTTGACACAGGTTTGGAGT 420 QY

361 AACTTGTIGAGAGGCTATIGAAAAATCATTTGIGCTTTTCAGCTTGCACACAGGTTTGGAGT 420

421 ATGCAACAGCTATAATTTTGCAAAAAGGAAAATAACTCTCCTGAACATCTAAAAGATG 480

DB 421 ATGCAACAGCTATAATTTCGAAAAAAGGAAAAATAACTCTCTGAAACATCTAAAAGATG 480

481 AAGTTTCTATCATCCAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540

481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540

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DB	601	CTGTGAGAACTCTTGAGGCAAAAGCAGCGGATACAACTCAAAGACGTCGTGTACACTTG	660
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DB	661	AAATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGGCAACTTTATTGCACTGTGGGAG	720
QY	721	ATCAGAAATGTTACAAATCACCCCTCAAGGAACCCAGGGATGAATACAGTTTGGATTTCTG	780
DB	721	ATCAGAAATGTTACAAATCACCCCTCAAGGAACCCAGGGATGAATACAGTTTGGATTTCTG	780
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DB	781	CAAAAAAGGCTGCTTGTGAAATTTTCTGAGACGGATGTAACAAAATCTGAAACATCATCAAC	840
QY	841	CCAGTAATAANTGATTTGNACACCACTGAGAGCGTGCAGCTGAGAGCATCCAGAAAGT	900
DB	841	CCAGTAATAANTGATTTGNACACCACTGAGAGCGTGCAGCTGAGAGCATCCAGAAAGT	900
QY	901	ATCAGGGTAGTTCTGTTTCAAACCTTGATGTGGAGCCATGTGGCACAAATACTCATGCCA	960
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DB	961	GCTCATTCACGATGAGNACAGCACTTATTACTCACTAAAGACAGAAATGAATGTAGAAA	1020
QY	1021	AGGCTGAAATTCGTATAAAGCAAAACAGCGCTTGTAGCAAGAGGCAACATACACAGAT	1080
DB	1021	AGGCTGAAATTCGTATAAAGCAAAACAGCGCTTGTAGCAAGAGGCAACATACACAGAT	1080
QY	1081	GGGCTGGAAGTAAGGAACACTGTAACTATAGGCGGACTCCCGCCACAGAAAAAAGGTAG	1140
DB	1081	GGGCTGGAAGTAAGGAACACTGTAACTATAGGCGGACTCCCGCCACAGAAAAAAGGTAG	1140
QY	1141	ATCTGAAATGCTGATCCCTGTGTGAGAGAAAAGAAATGGAATAAGCAGAAACTGCCATGCT	1200
DB	1141	ATCTGAAATGCTGATCCCTGTGTGAGAGAAAAGAAATGGAATAAGCAGAAACTGCCATGCT	1200
QY	1201	CAGAGAACTCTAGAGATACCTGAGAGTCTCCCTTGGATTAACACTTAATAGCAGCAATTCAGA	1260
DB	1201	CAGAGAACTCTAGAGATACCTGAGAGTCTCCCTTGGATTAACACTTAATAGCAGCAATTCAGA	1260
QY	1261	AAGTTAATGATGGTTTTCCAGAAAGTGATGAACCTGTTTAGTCTTGATGATCCACATGATG	1320
DB	1261	AAGTTAATGATGGTTTTCCAGAAAGTGATGAACCTGTTTAGTCTTGATGATCCACATGATG	1320
QY	1321	GGGAGTCTGAATCAAAATGCCAAGTAGCTGACTATGAGCGCTTCTTAATAGAGGTAGATG	1380
DB	1321	GGGAGTCTGAATCAAAATGCCAAGTAGCTGACTATGAGCGCTTCTTAATAGAGGTAGATG	1380
QY	1381	AATATTTCTGGTTCTTCAGAGAAAATGACTTACTGGCCAGTGTCTCTATGAGGCTTTAA	1440
DB	1381	AATATTTCTGGTTCTTCAGAGAAAATGACTTACTGGCCAGTGTCTCTATGAGGCTTTAA	1440
QY	1441	TATCTAAAGTGGAAGAGTTTCATCCCAATCTAGTAGAGAGTAATATTGAGACAAATAT	1500
DB	1441	TATCTAAAGTGGAAGAGTTTCATCCCAATCTAGTAGAGAGTAATATTGAGACAAATAT	1500
QY	1501	TTGGAAAACTATPCGAAGAAAGCGAGCTCCCAACTTTAAGCCATGTAACTGAAAAATC	1560
DB	1501	TTGGAAAACTATPCGAAGAAAGCGAGCTCCCAACTTTAAGCCATGTAACTGAAAAATC	1560
QY	1561	TAATTTATAGAGCATTTGTTACTGAGCCACAGATATAAGAGCGTCCCTCCACAAATA	1620
DB	1561	TAATTTATAGAGCATTTGTTACTGAGCCACAGATATAAGAGCGTCCCTCCACAAATA	1620
QY	1621	AATTTAAGCGTAAAGAGACCTACATCAGCGCTTCATCTGAGGATTTTATCAAGAAAG	1680
DB	1621	AATTTAAGCGTAAAGAGACCTACATCAGCGCTTCATCTGAGGATTTTATCAAGAAAG	1680

Qy	1681	CAGATTTGGCAGGTTCTCAAAAGACTCCTGAAATGATAAATCAGGGAACATAACCAACCGAGC	1741
Db	1681	CAGATTTGGCAGGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACATAACCAACCGAGC	1741
Qy	1741	AGAAATGGTCAAGTCATGAATATTAATAAGCTGGTCAATAGTGGTCTGGAATATAAAACCAAAAGGTGATT	1800
Db	1741	AGAAATGGTCAAGTCATGAATATTAATAAGCTGGTCAATAGTGGTCTGGAATATAAAACCAAAAGGTGATT	1800
Qy	1801	CTATTTCAGAAATGAGAAAAATCTTAACCCATAGAAATCACTCGAAAAAGAAATCTGCTTTTCA	1860
Db	1801	CTATTTCAGAAATGAGAAAAATCTTAACCCATAGAAATCACTCGAAAAAGAAATCTGCTTTTCA	1860
Qy	1861	AAAACCAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATTCGAATATAAATATCC	1920
Db	1861	AAAACCAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATTCGAATATAAATATCC	1920
Qy	1921	ACAAATTCAAAGCACTTAAAGAAATAGGCTGAGGAGAAAGTCTTTTACAGGCATATTC	1980
Db	1921	ACAAATTCAAAGCACTTAAAGAAATAGGCTGAGGAGAAAGTCTTTTACAGGCATATTC	1980
Qy	1981	ATGCGCTTGAACCTAGTAGTCACTAGTAAATCTTAAGCCCACTAAATGCTACATGAAATTCGAAA	2040
Db	1981	ATGCGCTTGAACCTAGTAGTCACTAGTAAATCTTAAGCCCACTAAATGCTACATGAAATTCGAAA	2040
Qy	2041	TTGATAGTTGTTCTAGCAGTCAAGACAGATATAAGAAAAAAGAAATGACAAATGCCAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTCAAGACAGATATAAGAAAAAAGAAATGACAAATGCCAGTCA	2100
Qy	2101	GGCACGACGAAACCTACAACTCATGAAAGGTAAGAAACCTGCAACTGGAGCCCAAGAGA	2160
Db	2101	GGCACGACGAAACCTACAACTCATGAAAGGTAAGAAACCTGCAACTGGAGCCCAAGAGA	2160
Qy	2161	GTAACAAAGCAAAATGAACAGACAAAGTAAAAAGACATGACAGTGTATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAAAGCAAAATGAACAGACAAAGTAAAAAGACATGACAGTGTATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAACAAATGCACTGTTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAAGAAAT	2280
Db	2221	AGTTAACAAATGCACTGTTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAAGAAAT	2280
Qy	2281	TTGTCAATCTGAGCTTCCAAAGAGAGAAAGAAAGAGAAACCTAGAGAAACAGTTTAAAGTGT	2340
Db	2281	TTGTCAATCTGAGCTTCCAAAGAGAGAAAGAAAGAGAAACCTAGAGAAACAGTTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTCTCTGTACTGTATATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTCTCTGTACTGTATATGGCACTCAGG	2460
Qy	2461	AAAGATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Db	2461	AAAGATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Qy	2521	GTGTGAGTCAGTGTGCAAGCTTTGAAAAACCCCAAGGGAATAATTCATGTTGTTTCCAAAG	2580
Db	2521	GTGTGAGTCAGTGTGCAAGCTTTGAAAAACCCCAAGGGAATAATTCATGTTGTTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACAGAAAGGCTTTTAAGTATCCATTGGGACATGAAGTTTAAACAGTTC	2640
Db	2581	ATAATAGAAATGACAGAAAGGCTTTTAAGTATCCATTGGGACATGAAGTTTAAACAGTTC	2640
Qy	2641	GGGAAAACAGCATAGAAAAATGGAAGAAAGTGAACCTTCATGCTCAGTATTTTGCAGAAATACAT	2700
Db	2641	GGGAAAACAGCATAGAAAAATGGAAGAAAGTGAACCTTCATGCTCAGTATTTTGCAGAAATACAT	2700
Qy	2701	TCAGGTTTTCABAGCCGCTCATTTGCTCTGTTTTCBAATCCAGGAATGCAAGAGG	2760
Db	2701	TCAGGTTTTCABAGCCGCTCATTTGCTCTGTTTTCBAATCCAGGAATGCAAGAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGCTCTTAAAGGAAACAAAGTCCAAAAGTCACATT	2820

D	b		2761	AATGTGCAACAGTCTCTGGCCACTCTGGTGCCCTTTAAAGGAACAAGAAGTCCAAAGAGTCACATT	2820
Q	y		2821	TTGAATGTGAACAAAAGGAAGAAAAATCNAGGAAGAATCAGTCTAATATATCAAGCCCTGTAC	2880
D	b		2821	TTGAATGTGAACAAAAGGAAGAAAAATCNAGGAAGAATCAGTCTAATATATCAAGCCCTGTAC	2880
Q	y		2881	AGACAGTTAATATCATCTGAGCGCTTCCTGTGTGTGTCAGAAAGATAAGCCAGTTGATA	2940
D	b		2881	AGACAGTTAATATCATCTGAGCGCTTCCTGTGTGTGTCAGAAAGATAAGCCAGTTGATA	2940
Q	y		2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTTCAGAGGCA	3000
D	b		2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTTCAGAGGCA	3000
Q	y		3001	ACGAAACTGAGCACTATTCTCCAAATAAACATGGACTTTTACAAAACCATAATGCTATAC	3060
D	b		3001	ACGAAACTGAGCACTATTCTCCAAATAAACATGGACTTTTACAAAACCATAATGCTATAC	3060
Q	y		3061	CACCACATTTTCCCACATCAGTCAATTTGTTAAABACTAAATGTAAGAAABAATCTGCTAGAGG	3120
D	b		3061	CACCACATTTTCCCACATCAGTCAATTTGTTAAABACTAAATGTAAGAAABAATCTGCTAGAGG	3120
Q	y		3121	AAAACTTTGAGGAACATTCCAATGCACCTGAAAGAGAAATGGGAAATGAGAACATTCCAA	3180
D	b		3121	AAAACTTTGAGGAACATTCCAATGCACCTGAAAGAGAAATGGGAAATGAGAACATTCCAA	3180
Q	y		3181	GTCAGTGTAGCACAANTTAGCCGTAAATAACATTAGAGAAAAATGTTTTAAAGAGCCAGCT	3240
D	b		3181	GTCAGTGTAGCACAANTTAGCCGTAAATAACATTAGAGAAAAATGTTTTAAAGAGCCAGCT	3240
Q	y		3241	CAAGCAATATAAATGAAGTAGGTTCCAGTAGTACTAATGMACTGGGCTCCAGTATTATGAAA	3300
D	b		3241	CAAGCAATATAAATGAAGTAGGTTCCAGTAGTACTAATGMACTGGGCTCCAGTATTATGAAA	3300
Q	y		3301	TAGGTTCCAGTGATGAAAAATTCAAGCAAGACTAGGTAGAAAACAGAGGGCCCCAAATTTGA	3360
D	b		3301	TAGGTTCCAGTGATGAAAAATTCAAGCAAGACTAGGTAGAAAACAGAGGGCCCCAAATTTGA	3360
Q	y		3361	ATGCTATGCTTAGATTAGGGTTTTTCCAACTCTGAGTCTATATAAACAAGTCTTCTCTGAA	3420
D	b		3361	ATGCTATGCTTAGATTAGGGTTTTTCCAACTCTGAGTCTATATAAACAAGTCTTCTCTGAA	3420
Q	y		3421	GTAATTTGAAGCATCTCTGAATAAAAAAGCAAGATATGAAGAAGTAGTTCAGACTGTTA	3480
D	b		3421	GTAATTTGAAGCATCTCTGAATAAAAAAGCAAGATATGAAGAAGTAGTTCAGACTGTTA	3480
Q	y		3481	ATACAGATTTCTCTCATAATCTGATTTTCAGATAAATTAGAAACAGCGCTATGGGAAGTAGTC	3540
D	b		3481	ATACAGATTTCTCTCATAATCTGATTTTCAGATAAATTAGAAACAGCGCTATGGGAAGTAGTC	3540
Q	y		3541	ATGCATCTCAGGTTTTCTTGAGACACCTGATGACTGTGTAGATGATGTGTAATAAAGG	3600
D	b		3541	ATGCATCTCAGGTTTTCTTGAGACACCTGATGACTGTGTAGATGATGTGTAATAAAGG	3600
Q	y		3601	AAGATCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTCTGTTTTTAGCAAAAGCG	3660
D	b		3601	AAGATCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTCTGTTTTTAGCAAAAGCG	3660
Q	y		3661	TCCAGAGAGAGAGCTTACGAGGTCCTTAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
D	b		3661	TCCAGAGAGAGAGCTTACGAGGTCCTTAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Q	y		3721	GTTPCCGAGAGGGGCCAAGAAATTAGAGTCTCTAGAAGAGAACTTATCTAGTGAAGATG	3780
D	b		3721	GTTPCCGAGAGGGGCCAAGAAATTAGAGTCTCTAGAAGAGAACTTATCTAGTGAAGATG	3780
Q	y		3781	AGAGAGCTCCCTGCTTCCCAACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
D	b		3781	AGAGAGCTCCCTGCTTCCCAACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
Q	y		3841	CTACTAGGCATGACCGGTGCTACCGAGTGTCTCTTAAGAAACACAGAGAGAAATTTAT	3900

3841	DB	CTACTAGGCATAGCACCGTGTCTACCGAGTGTCCTGTCTTAAGAACACACAGAGGAGAAATTAT	3901
3901	QY	TATCATTTCAAGAAATAGCTTAAATGACTGCAGTAACACAGGTAAATATTTGGCAAAAGGCATCTC	3960
3901	DB	TATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACACAGGTAAATATTTGGCAAAAGGCATCTC	3960
3961	QY	AGGAAACATCACCTTAGTGAGGAAACAAATGGTTCTGTAGCTTGTTTTCTTCACAGTGCA	4020
3961	DB	AGGAAACATCACCTTAGTGAGGAAACAAATGGTTCTGTAGCTTGTTTTCTTCACAGTGCA	4020
4021	QY	GTGAATTTGGAAGACTTGCACTGCAAAATACAAACACCCAGGATCCCTTCTTCATTTGGTTCTT	4080
4021	DB	GTGAATTTGGAAGACTTGCACTGCAAAATACAAACACCCAGGATCCCTTCTTCATTTGGTTCTT	4080
4081	QY	CCAAACAAATGAGGCHTCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGAACAAGAAATTTGG	4140
4081	DB	CCAAACAAATGAGGCHTCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGAACAAGAAATTTGG	4140
4141	QY	TTTCAGATGATGAAGAAAGGAGACCGGCTTTGGAAGAAATTAATCAAGAAGACCAAGCA	4200
4141	DB	TTTCAGATGATGAAGAAAGGAGACCGGCTTTGGAAGAAATTAATCAAGAAGACCAAGCA	4200
4201	QY	TGGATTCAAACTTAGGTGAAGAGCAGCATCTGGGTGTGAGTGAAGAAACAAGCGTCTCTGAAG	4260
4201	DB	TGGATTCAAACTTAGGTGAAGAGCAGCATCTGGGTGTGAGTGAAGAAACAAGCGTCTCTGAAG	4260
4261	QY	ACTGCTCAGGGCTATCCCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGGATACCATGCG	4320
4261	DB	ACTGCTCAGGGCTATCCCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGGATACCATGCG	4320
4321	QY	AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGTGTTGTAGAACAGC	4380
4321	DB	AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGTGTTGTAGAACAGC	4380
4381	QY	ATGGGAGCCAGGCTTCTAAACAGCTACCCCTTCATCATTAAGTGACTCTTCTGCCCTTTGAGG	4440
4381	DB	ATGGGAGCCAGGCTTCTAAACAGCTACCCCTTCATCATTAAGTGACTCTTCTGCCCTTTGAGG	4440
4441	QY	ACCTTGGGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACACAAAGTA	4500
4441	DB	ACCTTGGGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACACAAAGTA	4500
4501	QY	GTGNAATACCCATATAGCCAGAAATCCAGAGGCGCTTTCTGTGTGACAAAGTTTGAAGTGTCTG	4560
4501	DB	GTGAATACCCATATAGCCAGAAATCCAGAGGCGCTTTCTGTGTGACAAAGTTTGAAGTGTCTG	4560
4561	QY	CAGATAGTCTTACACAGTAAAAATAAGAACACAGGAGTGGAAAGGTCAATCCCTTCTTAAT	4620
4561	DB	CAGATAGTCTTACACAGTAAAAATAAGAACACAGGAGTGGAAAGGTCAATCCCTTCTTAAT	4620
4621	QY	GCCCATCATTTAGATGATAGGTGTACATGCACAGTTGCTCTTGGAGTCTTTCAGAAATAGAA	4680
4621	DB	GCCCATCATTTAGATGATAGGTGTACATGCACAGTTGCTCTTGGAGTCTTTCAGAAATAGAA	4680
4681	QY	ACTTACCATCTCAGAGGAGCTCATTAAGGTGTTCATGTGGAGGAGCAACAGCTCGAAG	4740
4681	DB	ACTTACCATCTCAGAGGAGCTCATTAAGGTGTTCATGTGGAGGAGCAACAGCTCGAAG	4740
4741	QY	AGTCTGGGCCACACGAATTTGACGGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGGAA	4800
4741	DB	AGTCTGGGCCACACGAATTTGACGGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGGAA	4800
4801	QY	CCCCCTTACCTGGAAATCTGGAAATCAGGCTCTTCTCTGATGATGACCCCTGAAATCTGATCTCTG	4860
4801	DB	CCCCCTTACCTGGAAATCTGGAAATCAGGCTCTTCTCTGATGATGACCCCTGAAATCTGATCTCTG	4860
4861	QY	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGTTGGCAACATACCATCTTCAACTCTGCAATTGA	4920
4861	DB	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGTTGGCAACATACCATCTTCAACTCTGCAATTGA	4920
4921	QY	AAGTTCCTCCAAATTTGAAGTTGCAAGATCTGTGCCACAGGGTCCAGTGTGCTCACTACTCTG	4980
4921	DB	AAGTTCCTCCAAATTTGAAGTTGCAAGATCTGTGCCACAGGGTCCAGTGTGCTCACTACTCTG	4980

Qy	4981	ATAC	TGCTGGGTATATAGCAATGGAAGAAAGTGTGAGAGGGAGAGACCGAGAATTTGCACAG	5040
Db	4981	ATACTG	TCTGGGTATATAGCAATGGAAGAAAGTGTGAGAGGGAGAGACCGAGAATTTGCACAG	5040
Qy	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTC	CAATGGTGGTGTCTGGCGCTGCACCCCAAGAG	5100
Db	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTC	CAATGGTGGTGTCTGGCGCTGCACCCCAAGAG	5100
Qy	5101	AAITTAATGCTGCTGATCAAGTTTGCCCGA	AAAAACAACAATCACTTTTAACTTAATCTAATTA	5160
Db	5101	AAITTAATGCTGCTGATCAAGTTTGCCCGA	AAAAACAACAATCACTTTTAACTTAATCTAATTA	5160
Qy	5161	CTGAAGAGACTACTCAATGTTTATGAA	AAACAGATGCTGAGTTTGTGTGGAACGACAC	5220
Db	5161	CTGAAGAGACTACTCAATGTTTATGAA	AAACAGATGCTGAGTTTGTGTGGAACGACAC	5220
Qy	5221	TGAAATATTTTCTAGGAATTCGGGAG	AGAAAAATGGGTAGTTACTATTTCTGGTGAACCC	5280
Db	5221	TGAAATATTTTCTAGGAATTCGGGAG	AGAAAAATGGGTAGTTACTATTTCTGGTGAACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATGCTCA	ATGAGATGATTTTGAAAGTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATGCTCA	ATGAGATGATTTTGAAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAAACCAACAGAGTCC	AAAGCGAGAGAAATCCCAAGGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACAGAGTCC	AAAGCGAGAGAAATCCCAAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGGCTAGAAATCTGTTGGTAT	TGGGCCCTTTCACCAACATGCCCAACAGATCAACTGG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTTGGTAT	TGGGCCCTTTCACCAACATGCCCAACAGATCAACTGG	5460
Qy	5461	AATGGATGTTACAGCTGTGTGTGCTT	CTGTGGTGAAGAGCTTTCATCATTCACCCCTTG	5520
Db	5461	AATGGATGTTACAGCTGTGTGTGCTT	CTGTGGTGAAGAGCTTTCATCATTCACCCCTTG	5520
Qy	5521	GCACAGGTGCCACCAATTTGCTGGT	GTGCAGCCAGATGCTTGGACAGAGGACAATGGCT	5580
Db	5521	GCACAGGTGCCACCAATTTGCTGGT	GTGCAGCCAGATGCTTGGACAGAGGACAATGGCT	5580
Qy	5581	TCCATGCAATTTGGGCGAGATGTGTG	AGGCACTGTGACCCGAGAGTGGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGGCGAGATGTGTG	AGGCACTGTGACCCGAGAGTGGGTGTGGACA	5640
Qy	5641	GTGTAGCACTCTACCAAGTGCAGAG	AGCTGGAACCTTACTGATACCCCAAGATCCCCCA	5700
Db	5641	GTGTAGCACTCTACCAAGTGCAGAG	AGCTGGAACCTTACTGATACCCCAAGATCCCCCA	5700
Qy	5701	GCCACTACTGA	5711	
Db	5701	GCCACTACTGA	5711	

RESULT 12

AAV46471

ID AAV46471 standard; cDNA; 5711 BP.

XOXO

AC AAV46471;

DT 18-NOV-1998 (first entry)

[illegible]

DE Human BRCA1 omi3 polymorphism #7 cDNA.

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KW BRCA1; omil;
KW nol:mcmb:omil;

RW polymorphism; susceptibility; anti-
chromosome 17q: cc

XX chromosome 17q; ss.

Homo sapiens

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FT variation /product= "BRCA1 omi3 protein"
FT 4956 /*tag= b
FT /note= "This polymorphic variation can be an A or G
FT /nucleotide"
XX US5750400-A.
XX
XX PD 12-MAY-1998.
XX
XX PF 12-FEB-1997; 97US-00798691.
XX
XX PR 12-FEB-1996; 96US-00598591.
XX
XX PA (ONCO-) ONCORMED INC.
XX
XX P1 Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC,
XX P2 Critz BS;
XX
XX PS WPI; 1998-296774/26.
XX
XX PT BRCA1 omi gene coding sequences - useful for distinguishing between
XX PT polymorphisms and mutation(s) in the screening for disposition to breast
XX PT or ovarian cancer.
XX
XX PS Claim 2e; Page: 54pp; English.
XX
XX CC This sequence encodes a human BRCA1 (breast and ovarian cancer
XX CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
XX CC nucleotide 4956. This sequence and other polymorphic variations of this
XX CC sequence are useful for the identification of an individual who may or
XX CC may not have an increased susceptibility to breast or ovarian cancer. The
XX CC sequences used identify gene changes which are due to polymorphisms,
XX CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX CC suppressor) which is involved in genetic inheritance of cancers,
XX CC especially breast and ovarian cancer. It is found at human chromosome 17q
XX CC which is known to be linked to cancer susceptibility, especially breast
XX CC cancer. Cells containing a mutation in this gene lose the wild-type
XX CC function of BRCA1 and are more susceptible to cancers. NOTE: This
XX CC sequence does not appear in the specification but has been created from
XX CC the wild type BRCA1 omi3 gene represented in AAV46450
XX
XX SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB |||||||

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D	b	2281	TTGTCATCTTAGCTTCCAAAGAGAGAAAGAGAGAGAACTAGAGAAACAGTTAAAGTGT	2340
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D	b	2401	AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACTTGTATGATTAAGCACTCAGG	2460
Q	y	2461	AAAGATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCCAAATAAT	2520
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Q	y	2521	GTGTGAGTCAGTGTGAGCAATTTGA AAAACCCCAAGGGAATAATCATGTTGTTCCAAAG	2580
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RESULT 13
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AC AAT87085;

XX 06-JAN-1998 (first entry)
 XX Human BRCA1 gene consensus.
 XX BRCA1 gene; BRCA1 (oni); breast cancer; ovary cancer; polymorphism;
 KW genetic testing; diagnosis; gene therapy; ss.
 XX Homo sapiens.
 XX
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 XX 12-FEB-1996; 96US-00598591.
 XX
 XX 12-FEB-1996; 96US-00598591.
 XX
 XX (ONCO-) ONCORMED INC.
 XX
 XX Olson SJ, Allen AC, Zeng B, Schelter DB, Alvares CP, Murphy PD;
 PI Critz BS;
 XX WPI; 1997-401843/37.
 DR P-PSDB; AAW26522.
 XX
 XX Human BRCA1 gene coding sequence with common normal polymorphisms - for
 PT assessing susceptibility to breast or ovarian cancer.
 XX
 XX Claim 1; Col 19-24; 35pp; English.
 XX
 XX This nucleotide sequence comprises a consensus DNA sequence, designated
 CC BRCA1 (oni), for the normal human BRCA1 gene. It was found by end-to-end
 CC sequencing of the BRCA1 gene from 5 individuals randomly drawn from the
 CC population and found to have no family history of breast or ovarian
 CC cancer. The BRCA1 (oni) gene and the seven polymorphic sites (which are
 CC not associated with breast or ovarian cancer) will provide greater
 CC accuracy and reliability for genetic testing. A claimed method for
 CC detecting an increased genetic susceptibility to breast and ovarian
 CC cancer resulting from the presence of a mutation in the BRCA1 coding
 CC sequence involves amplifying and sequencing the BRCA1 coding sequence

CC from an individual and comparing the sequence with BRCA1 (oni). The
 CC consensus normal BRCA1 sequence can also be used in gene therapy, to make
 CC diagnostic probes and to express normal BRCA1 polypeptide (see AAW26522)
 XX
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;
 Query Match 100.0%; Score 5709.4; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 AGCTCGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60
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 DB 61 CTTGGCGTCAAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTCAATTTGGAAACAGAAAGAA 120
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 DB 121 TGGATTATCTGCTCTTTCGGTTGAAGAAGTACAAATGTCAATTAATGCTATGCAGAAAA 180
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 DB 841 CCAGTAATATGATTGAAACCACTGAGAGAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900
 QY 901 ATCAGGATAGTCTGTCTTCAAACTTGCATGTGGAGCCATGTGGCACAAAATCTCATGCCA 960
 DB 901 ATCAGGATAGTCTGTCTTCAAACTTGCATGTGGAGCCATGTGGCACAAAATCTCATGCCA 960

QY 961 GCTCATTTACAGCATGAGAACAGCAGCTTTATTACTCACTAAAGACAGAAATGAATGTAGAAA 1020
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QY 1021 AGGCTGAATCTTGTAATAAAGCAACACAGCTGGCTTAGCAGAGGAGCCAAATACAGAT 1080
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QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATAACACTAATAGCAGCATTCAGA 1260
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 DB 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTTGACCCGAGAGTGGTGTGGACA 5640
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 QY 5701 GCCACTACTGA 5711
 DB 5701 GCCACTACTGA 5711

RESULT 14
 ID AAV46448 standard; cDNA; 5711 BP.

AC AAV46448;

DT 18-NOV-1998 (first entry)

XX Human BRCA1 omil cDNA.

XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 XX chromosome 17q; ss.

XX Homo sapiens.

Key Location/Qualifiers
 CDS 120..5711
 /*tag= a
 /product= "BRCA1 omil protein"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-00798591.

XX 12-FEB-1996; 96US-00598591.

XX (ONCO-) ONCORMED INC.

XX Olsson SJ, Murphy, PD, Zeng B, Alvares CP, Schelter DB, Allen AC;
 XX Critz BS;

XX WPI; 1998-296774/26.

XX P-PSDB; AAW76098.

XX BRCA1 omi gene coding sequences - useful for distinguishing between
 XX polymorphisms and mutation(s) in the screening for disposition to breast
 XX or ovarian cancer.

XX Claim 2d; Col 27-32; 54pp; English.

XX

CC This sequence encodes the human BRCA1 (breast and ovarian cancer
 CC predisposing gene) omil gene. This sequence and polymorphic variations of
 CC this sequence are useful for the identification of an individual who may
 CC or may not have an increased susceptibility to breast or ovarian cancer.
 CC The sequences used identify gene changes which are due to polymorphisms,
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 CC suppressor) which is involved in genetic inheritance of cancers,
 CC especially breast and ovarian cancer. It is found at human chromosome 17q
 CC which is known to be linked to cancer susceptibility, especially breast
 CC cancer. Cells containing a mutation in this gene lose the wild-type
 CC function of BRCA1 and are more susceptible to cancers
 XX

SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;

Query Match 100.0%; Score 5709.4; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGACCCCGCAGCCGCTGTGGGTTCTCAGATAACTGGGCC 60
 DB 1 AGCTCGCTGAGACTTCTCGACCCCGCAGCCGCTGTGGGTTCTCAGATAACTGGGCC 60
 QY 61 CTTGCGCTCAGGAGGCTTTCACCTCTGCTCTGGGTAAAGTTTCATTGGAAACAGAAAGAA 120
 DB 61 CTTGCGCTCAGGAGGCTTTCACCTCTGCTCTGGGTAAAGTTTCATTGGAAAGAAAGAA 120
 QY 121 TGGATTTATCTGCTCTTTCGGGTTGAAAGATACAAATGTCTAATATGTCATGACAGAAA 180
 DB 121 TGGATTTATCTGCTCTTTCGGGTTGAAAGATACAAATGTCTAATATGTCATGACAGAAA 180
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 DB 181 TCTTAGAGTGTCCATCTGCTGAGTTCATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
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 DB 241 ACATATTTTGCATAATTTTGCATCTGCTGCTCAACCCAGAGAAAGGCGCTTCACAGT 300
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 DB 541 AACCCGAAATTCCTTCTGAGGAAACAGTCTCAGTGTCCAACTCTTACCTTGGAA 600
 QY 601 CTGTGAGAACTCTGAGGACAAAGAGGAGTACAACTCTCAAGAGAGCTGTCTACATG 660
 DB 601 CTGTGAGAACTCTGAGGACAAAGAGGAGTACAACTCTCAAGAGAGCTGTCTACATG 660
 QY 661 AATGGGATCTGATTTCTTGAAGATACCGTTTAAATAGGCAACTTATTTCAGTGTGGAG 720
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 DB 721 ATCAGAGATCTTACAAATCCCTCAAGAAACAGGAGTGAATTCAGTTTGGATCTG 780
 QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGAGTGAACAAATATCAATCATCAAC 840
 DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGAGTGAACAAATATCAATCATCAAC 840

QY 841 CCAGTAATAATGATTGTAACACCACTGAGAGAGCGTGCAGCTCAGAGGCGATCCAGAAAAGT 900
DB 841 CCAGTAATAATGATTGTAACACCACTGAGAGAGCGTGCAGCTCAGAGGCGATCCGAAAAGT 900
QY 901 ATCAGGGTAGTTCCTGTTTCAAACTTGCGATGTGGAGCCCATGTGGCCCAAAATCTCATGCCA 960
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DB 1741 AGAATGCTAAGTGATGAATTAATTAATGATGCTCATGAGAAATAAAGAGGTGAT 1800
QY 1801 CTATTCAGAAATGAGAAAATCTTAACCCATAGAACTCACTCGAAAAAGATCTGTTTCA 1860
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QY 1861 AAACGAAAGCTGAACCTTATAGCAGGAGTATAGCAATATGGAATCGAATTAATATCC 1920
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QY 1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGAGGAAAGTCTTCTACAGGCGATATTC 1980
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Db 3901 TATCATTTGAAGATAGCTTTAATGACTCTGATTAACCTAGGTTAATTTGCAAGGCAATCTC 3960
Qy 3961 AGGAACATCACTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTCACAGTGCA 4020
Db 3961 AGGAACATCACTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTCACAGTGCA 4020
Qy 4021 GTGAATTTGAGAGCTTCTGCTCAATATACACACCCAGGATCTTTCTTCAATGTTGTTCT 4080
Db 4021 GTGAATTTGAGAGCTTCTGCTCAATATACACACCCAGGATCTTTCTTCAATGTTGTTCT 4080
Qy 4081 CCAAAACAAATGAGGCAATCAGTCTGAAAGCCAGGAGTTGCTGTGAGTGAACAGGAATGG 4140

Db 4081 CCAAAACAAATGAGGCAATCAGTCTGAAAGCCAGGAGTTGCTGTGAGTGAACAGGAATGG 4140
Qy 4141 TTTTCAGTGTATGAAGAAAGAGAAAGCGCTTTGGAAAGAAAATAATCAAGAAAGCAAGCA 4200
Db 4141 TTTTCAGTGTATGAAGAAAGAGAAAGCGCTTTGGAAAGAAAATAATCAAGAAAGCAAGCA 4200
Qy 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAAG 4260
Db 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAAG 4260
Qy 4261 ACTGCTCAGGGGTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGGGTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATGC 4320
Qy 4321 AACATAACCTCATATAAGCTCCAGCAGGAAATGGCTGTGAACCTAGAGTGAAGTGTGTGAACAGC 4380
Db 4321 AACATAACCTCATATAAGCTCCAGCAGGAAATGGCTGTGAACCTAGAGTGAAGTGTGTGAACAGC 4380
Qy 4381 ATGGAGCCAGCTTTCTAAACAGCTACCTTTCCATCATAGTGAACCTTTCTGCCCCCTTGAGG 4440
Db 4381 ATGGAGCCAGCTTTCTAAACAGCTACCTTTCCATCATAGTGAACCTTTCTGCCCCCTTGAGG 4440
Qy 4441 ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAGCAGTATTAACCTTCAGAAAAGTA 4500
Db 4441 ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAGCAGTATTAACCTTCAGAAAAGTA 4500
Qy 4501 GTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTGCTG 4560
Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTGCTG 4560
Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGGAAAGGTCTATCCCTTCTTAAT 4620
Db 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGGAAAGGTCTATCCCTTCTTAAT 4620
Qy 4621 GCCCATCATTTAGATGATAGTGTGTACATGACAGTCTCTGCTGGAGTCTTCAGAAATAGAA 4680
Db 4621 GCCCATCATTTAGATGATAGTGTGTACATGACAGTCTCTGCTGGAGTCTTCAGAAATAGAA 4680
Qy 4681 ACTACCCATCTCAGAGGAGCTCATTTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAG 4740
Db 4681 ACTACCCATCTCAGAGGAGCTCATTTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAG 4740
Qy 4741 AGTCTGGGCCACACAGATTTGACGGAACATCTTACTTGCACAGCAGATCTAGAGGGA 4800
Db 4741 AGTCTGGGCCACACAGATTTGACGGAACATCTTACTTGCACAGCAGATCTAGAGGGA 4800
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCTG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCTG 4860
Qy 4861 AAGACAGAGCCCGAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920
Db 4861 AAGACAGAGCCCGAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920
Qy 4921 AAGTTCCTCCAAATTTGAAAGTTGCAAGATCTGCCCAGGCTCCAGCTGCTGCTCATCTACTG 4980
Db 4921 AAGTTCCTCCAAATTTGAAAGTTGCAAGATCTGCCCAGGCTCCAGCTGCTGCTCATCTACTG 4980
Qy 4981 ATACTCTCTGGTATATATGCAATGGAAGAAAGTGTGAGCAGGGAGAGGCAAGATTCACAG 5040
Db 4981 ATACTCTCTGGTATATATGCAATGGAAGAAAGTGTGAGCAGGGAGAGGCAAGATTCACAG 5040
Qy 5041 CTTTCAACAGAAAAGGTTCAACAAAAGAAATGCTCCATGTTGGTGTCTGGCCCTGAGCCCAAGAG 5100
Db 5041 CTTTCAACAGAAAAGGTTCAACAAAAGAAATGCTCCATGTTGGTGTCTGGCCCTGAGCCCAAGAG 5100
Qy 5101 AATTTATGCTGTGATCAAGTTTGCAGAAAACACACATCACTTTTAACTAATTA 5160
Db 5101 AATTTATGCTGTGATCAAGTTTGCAGAAAACACACATCACTTTTAACTAATTA 5160
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTTGTTGAGCCGACAC 5220
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTTGTTGAGCCGACAC 5220

QY 5221 TCAAAATATTTCTAGCAATTCGGGAGGAGAAATGGGTAGTTAGTCTATTTCTGGGTGACCC 5280
 Db 5221 TCAAAATATTTCTAGCAATTCGGGAGGAGAAATGGGTAGTTAGTCTATTTCTGGGTGACCC 5280
 QY 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCAGATTTTGAAGTCAGAGAGATGCG 5340
 Db 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCAGATTTTGAAGTCAGAGAGATGCG 5340
 QY 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCCGAGCAAGAGAAATCCCAAGCAGAGAAAGATCT 5400
 Db 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCCGAGCAAGAGAAATCCCAAGCAGAGAAAGATCT 5400
 QY 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCACCAATGCCCAAGATCAATCTGG 5460
 Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCACCAATGCCCAAGATCAATCTGG 5460
 QY 5461 AATGATGCTACAGCTGTGTTGCTTCTGTTGTTGAGGAGCTTTCATCTTCACTCCCTTG 5520
 Db 5461 AATGATGCTACAGCTGTGTTGCTTCTGTTGTTGAGGAGCTTTCATCTTCACTCCCTTG 5520
 QY 5521 GCACAGGTGTCACCAATCTGTTGTTGTTGAGGAGCTTTCATCTTCACTCCCTTG 5580
 Db 5521 GCACAGGTGTCACCAATCTGTTGTTGTTGAGGAGCTTTCATCTTCACTCCCTTG 5580
 QY 5581 TCCATGCAATGGGCGAGATGTTGAGGCACTGTGTTGTTGAGGAGCTTTCATCTTCACTCCCTTG 5640
 Db 5581 TCCATGCAATGGGCGAGATGTTGAGGCACTGTGTTGTTGAGGAGCTTTCATCTTCACTCCCTTG 5640
 QY 5641 GTGTAGCACTTACAGTGCAGAGCTGAGCACTTACCTGATACCCAGATCCCCACCA 5700
 Db 5641 GTGTAGCACTTACAGTGCAGAGCTGAGCACTTACCTGATACCCAGATCCCCACCA 5700
 QY 5701 GCCACTACTGA 5711
 Db 5701 GCCACTACTGA 5711

RESULT 15

AAV62180
 ID AAV62180 standard; DNA; 5711 BP.

AC AAV62180;

DT 11-FEB-1999 (first entry)

XX BRCA1 (omil) coding sequence.

XX BRCA1; mutation detection; disease screening; multiple allele variation;
 XX Breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;
 XX Duchenne muscular dystrophy; Becker muscular dystrophy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 120..5711
 XX /*Cag= a

PN W09844157-A2.

XX 08-OCT-1998.

XX 26-MAR-1998; 98NC-US006002.

XX 28-MAR-1997; 97US-00825487.

XX (ONCO-) ONCORMED INC.

XX Murphy PD, White MB;

XX WPI; 1998-542713/46.

XX P-PSDB; AAW79665.

XX

Identifying variations in polynucleotide sequences - using allele specific hybridisation assay, sequence variation locating assay, and direct sequencing, in a stepwise procedure.

Disclosure; Fig 1a-j; 62pp; English.

This sequence encodes the human BRCA (omil) protein, and was used to test the method of the invention. The method is for determining the presence or absence of a sequence variation in a gene sample, and comprises: (a) performing an allele specific hybridisation assay for one or more pre-determined sequence variations; (b) if no pre-determined sequence variation found in step (a) then performing a sequence variation location assay; (c) if no sequence variation found in step (b) then sequencing the gene sample; (cii) if sequence variation is found in step (b) then the targeted confirmatory sequencing is performed; and (d) determining the presence of a sequence variation by analysing the sequence(s) obtained in step (cii) or step (cii) against a reference sample. Alternatively, step (a) or step (b) is omitted from the method. The invention provides a stepwise and integrated method for the efficient and accurate detection of variations in polynucleotide sequences, being directed towards screening for diseases associated with multiple allele variations, including breast and ovarian cancer, cystic fibrosis, Duchenne and Becker muscular dystrophy, and Li-Fraumeni syndrome

Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;

Query Match 100.0%; Score 5709.4; DB 2; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTGTGACCCGCCACAGGCTCTGGGGTTCTCAGATAACTGGCC 60
 Db 1 AGCTCGCTGAGACTTCTGTGACCCGCCACAGGCTCTGGGGTTCTCAGATAACTGGCC 60
 QY 61 CTGCGCTCAGGAGGCTTCACTCTGCTCTGGGTAAGTTTCATTGGACAGAAAGAA 120
 Db 61 CTGCGCTCAGGAGGCTTCACTCTGCTCTGGGTAAGTTTCATTGGACAGAAAGAA 120
 QY 121 TGGATTATCTGCTCTGCGGTGAGAGAGTCAAAATCTCATTATGCTATGACAGAAA 180
 Db 121 TGGATTATCTGCTCTGCGGTGAGAGAGTCAAAATCTCATTATGCTATGACAGAAA 180
 QY 181 TCTTAGAGTGTCCATCTCTGCGAGTTTCATCAAGGAACTGTCTCCACAAAGTGTGACC 240
 Db 181 TCTTAGAGTGTCCATCTCTGCGAGTTTCATCAAGGAACTGTCTCCACAAAGTGTGACC 240
 QY 241 ACATATTTGCAAAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGGCTTCAAGT 300
 Db 241 ACATATTTGCAAAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGGCTTCAAGT 300
 QY 301 GTCCCTTATGTAAAGATGATATAACCAAAAGGAGCTCAAGAAAGTACAGATTAGTC 360
 Db 301 GTCCCTTATGTAAAGATGATATAACCAAAAGGAGCTCAAGAAAGTACAGATTAGTC 360
 QY 361 AACTTGTGAAGAGCTATTTGAAAATCATTTGTGCTTTTTCAGCTTCAACAGATTAGT 420
 Db 361 AACTTGTGAAGAGCTATTTGAAAATCATTTGTGCTTTTTCAGCTTCAACAGATTAGT 420
 QY 421 ATGCAAAACAGCTATAATTTTGCAAAAGGAAATTAAGTCTCTCTGAAATCTTAAAGATG 480
 Db 421 ATGCAAAACAGCTATAATTTTGCAAAAGGAAATTAAGTCTCTCTGAAATCTTAAAGATG 480
 QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGATG 540
 Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGATG 540
 QY 541 AACCCGAAATCTCTTCTTGGAGGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
 Db 541 AACCCGAAATCTCTTCTTGGAGGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
 QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTGTCTACATG 660
 Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTGTCTACATG 660

QY 661 AATTGGGATCTGATCTCTCTGAGATACCGTTTAAATAAGGCAACTTATTGCGGTGGGAG 720
DB 661 AATTGGGATCTGATCTCTCTGAGATACCGTTTAAATAAGGCAACTTATTGCGGTGGGAG 720
QY 721 ATCAAGAATTGTGTACAAATCAACCCCTCAAGAGAACCAAGGATCAAAATCAGTTTGGATTCTG 780
DB 721 ATCAAGAATTGTGTACAAATCAACCCCTCAAGAGAACCAAGGATCAAAATCAGTTTGGATTCTG 780
QY 781 CAAAAAGGCTCTGTTGAAATTTCTGAGACCGATGTAACAAATCTGACATCATCAAC 840
DB 781 CAAAAAGGCTCTGTTGAAATTTCTGAGACCGATGTAACAAATCTGACATCATCAAC 840
QY 841 CCAGTAATAATGATTGTAACCACTGAGAACCGTGCAGCTGAGAGGCATCCAGAAAAAT 900
DB 841 CCAGTAATAATGATTGTAACCACTGAGAACCGTGCAGCTGAGAGGCATCCAGAAAAAT 900
QY 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960
DB 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960
QY 961 GCTCAATACAGCATGAGAACAGCAGCTTTATTACTCACTAAAGACAGAAATGATGTAGAAA 1020
DB 961 GCTCAATACAGCATGAGAACAGCAGCTTTATTACTCACTAAAGACAGAAATGATGTAGAAA 1020
QY 1021 AGGCTGAATTTCTGTAATAAGCAAAACAGCCCTGCTTACGAGGAGCCAACTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATAAGCAAAACAGCCCTGCTTACGAGGAGCCAACTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAGCAAAATGATGATAGCGGACTCCAGCACAGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAGCAAAATGATGATAGCGGACTCCAGCACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAAGCAAGAACTGCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAAGCAAGAACTGCCATGCT 1200
QY 1201 CAGAGAACTCTAGAGATACCTGAAGATGTTCTTGGATTAACCTAAATAGCAGCACTTCA 1260
DB 1201 CAGAGAACTCTAGAGATACCTGAAGATGTTCTTGGATTAACCTAAATAGCAGCACTTCA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAATCTGTAGTGTCTGATCACTCAATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGAATCTGTAGTGTCTGATCACTCAATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGATGTTTGGAGCTTCTAAATGAGGTAGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGATGTTTGGAGCTTCTAAATGAGGTAGATG 1380
QY 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440
DB 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCAGTAGAGGTAAATATTGAGAGCAAAATAT 1500
DB 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCAGTAGAGGTAAATATTGAGAGCAAAATAT 1500
QY 1501 TTGGGAAACCTATCGGAGAGGCAAGCCTCCCAACTTAAGCCATGTAAGTCAAAATC 1560
DB 1501 TTGGGAAACCTATCGGAGAGGCAAGCCTCCCAACTTAAGCCATGTAAGTCAAAATC 1560
QY 1561 TAATATAGGAGCAATTTGTTACTGAGCCACAGATTAACAAGAGGCTCCCTCAAAATA 1620
DB 1561 TAATATAGGAGCAATTTGTTACTGAGCCACAGATTAACAAGAGGCTCCCTCAAAATA 1620
QY 1621 AATTAAGCGTAAAGGAGACTACATCAGGCTTCTGAGGATTTTATCAAGAAAG 1680
DB 1621 AATTAAGCGTAAAGGAGACTACATCAGGCTTCTGAGGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTAAACCAACGGAGC 1740
DB 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTAAACCAACGGAGC 1740

QY 1741 AGAATGGTCAAGTCTGATGAATATTACTAATAGTGGTCAATGAGAAATAAAACAAAAGGTGATT 1800
DB 1741 AGAATGGTCAAGTCTGATGAATATTACTAATAGTGGTCAATGAGAAATAAAACAAAAGGTGATT 1800
QY 1801 CTATTCAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAAGAAATCTCTTTCA 1860
DB 1801 CTATTCAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAAGAAATCTCTTTCA 1860
QY 1861 AAACGAAAGCTGAACTTATAAGCAGCAGTATAAGCAATATGGAATCTCGAATTAATATCC 1920
DB 1861 AAACGAAAGCTGAACTTATAAGCAGCAGTATAAGCAATATGGAATCTCGAATTAATATCC 1920
QY 1921 ACAATTCAAAAGCACCCTAAAGAAATAGGCTGAGAGGAAAGTCTTCTACCAAGGCATATTC 1980
DB 1921 ACAATTCAAAAGCACCCTAAAGAAATAGGCTGAGAGGAAAGTCTTCTACCAAGGCATATTC 1980
QY 1981 ATGCGCTTGAACCTAGTAGTAGTAAGTAATCTAAGCCCACTAAATGTTACTGAAATTCGAAA 2040
DB 1981 ATGCGCTTGAACCTAGTAGTAGTAAGTAATCTAAGCCCACTAAATGTTACTGAAATTCGAAA 2040
QY 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCGAGTCA 2100
DB 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCGAGTCA 2100
QY 2101 GGCAACAGCAAAACCTTACAACCTCACTGGAAGGTAAAGAACCTGCAACTGGAGCCAGAGA 2160
DB 2101 GGCAACAGCAAAACCTTACAACCTCACTGGAAGGTAAAGAACCTGCAACTGGAGCCAGAGA 2160
QY 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGTACTTTCGCCAGAGCTGA 2220
DB 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGTACTTTCGCCAGAGCTGA 2220
QY 2221 AGTTAACAATGCACTGCTGTTCTTTTACTAAGTGTTCAAAATACCAAGTGAACCTTAAAGAA 2280
DB 2221 AGTTAACAATGCACTGCTGTTCTTTTACTAAGTGTTCAAAATACCAAGTGAACCTTAAAGAA 2280
QY 2281 TTGTCAATCTCTAGCTTCCCAAGAGAGAAAAAGAGAAACTTAGAAAAACAGTTTAAAGTGT 2340
DB 2281 TTGTCAATCTCTAGCTTCCCAAGAGAGAAAAAGAGAAACTTAGAAAAACAGTTTAAAGTGT 2340
QY 2341 CTAAATATGCTGAAGCCCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGCAACTG 2400
DB 2341 CTAAATATGCTGAAGCCCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGCAACTG 2400
QY 2401 AAAGATCTGAGAGAGTAGCAGTATTCTACTGCTAGCTGCTGATTAAGGCACTCAGG 2460
DB 2401 AAAGATCTGAGAGAGTAGCAGTATTCTACTGCTAGCTGCTGATTAAGGCACTCAGG 2460
QY 2461 AAAGTATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAAACCAATAAAT 2520
DB 2461 AAAGTATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAAACCAATAAAT 2520
QY 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGACTTAAATCATGTTGTTCCAAAG 2580
DB 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGACTTAAATCATGTTGTTCCAAAG 2580
QY 2581 ATAAATGAAATGACACAGAGAGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640
DB 2581 ATAAATGAAATGACACAGAGAGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640
QY 2641 GGGAAACAGCATAGAAAATGGAAAGAGTGAATCTGATGCTCAGTATTTCGAGAAATACAT 2700
DB 2641 GGGAAACAGCATAGAAAATGGAAAGAGTGAATCTGATGCTCAGTATTTCGAGAAATACAT 2700
QY 2701 TCAAGGTTTCAAGCCGAGTCAATTTGCTCTGTTTCAATCCAGAAATGCAAGAGAGG 2760
DB 2701 TCAAGGTTTCAAGCCGAGTCAATTTGCTCTGTTTCAATCCAGAAATGCAAGAGAGG 2760
QY 2761 AATGTGCAATCTCTGCGCCACTCTGGGTCTTTAAAGAAAAAAGTCCAAAAGTCACTT 2820
DB 2761 AATGTGCAATCTCTGCGCCACTCTGGGTCTTTAAAGAAAAAAGTCCAAAAGTCACTT 2820
QY 2821 TTGAATGTGACAAACAAAGAGAGAAAAATCAAGGAAAGAAATGAGTCTAATATATCAAGCCTGTAC 2880

QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGGTGGTCTGGCCCTGACCCGAGAAG 5100
 DB |||||
 QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGGTGGTCTGGCCCTGACCCGAGAAG 5100
 DB |||||
 QY 5101 AATTATGTCGTGTACAAAGTTGGCAGAAACACCAATCATCTTTAACTAATCTAATTA 5160
 DB |||||
 QY 5101 AATTATGTCGTGTACAAAGTTGGCAGAAACACCAATCATCTTTAACTAATCTAATTA 5160
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 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTTGTTGAACGAGAC 5220
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 QY 5221 TCAATATATTTCTAGGAATGCGGAGAGAAATGCGTAGTAGCTATTTCTGGGTGACCC 5280
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 QY 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGGAGATGCG 5340
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 QY 5341 TCAATGGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400
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 QY 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCACAGATCAACTGG 5460
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 QY 5461 AATGATGATACAGCTGTGTGCTCTGTTGTTGAAGAGCTTTTCATCATTCACCCCTTG 5520
 DB |||||
 QY 5461 AATGATGATACAGCTGTGTGCTCTGTTGTTGAAGAGCTTTTCATCATTCACCCCTTG 5520
 DB |||||
 QY 5521 GCACAGGTGTCACCCCAATTTGTTGTCAGCCAGATGCCCTGGACAGAGGACATGGCT 5580
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 DB |||||
 QY 5641 GTGTAGCACTCTACAGTCCAGGAGCTGGACACTTACTGATACCCAGATGCCCCACA 5700
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 QY 5641 GTGTAGCACTCTACAGTCCAGGAGCTGGACACTTACTGATACCCAGATGCCCCACA 5700
 DB |||||
 QY 5701 GCCACTACTGA 5711
 DB |||||
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 DB |||||

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 Job time : 2019 secs